from the chromosome via a second recombination event over the duplicated target gene sequence either completed the allelic exchange or reconstituted the wild-type genotype. Subsequent loss of the plasmid in the absence of antibiotic selection pressure resulted in an erythromycin-sensitive phenotype. In order to assess gene replacement a screening of erythromycin-sensitive colonies was performed by analysis of the target gene PCR amplicons.

FIGURE 7 reports a schematic of the IS-1 operon for each knock-out strain generated, along with the deletion position within the amino acidic sequence. Most data presented here concern the COH1 deletion strains, in which the expression of each of the antigens is higher by DNA microarray analysis (data not shown) as well as detectable by FACS analysis (see FIGURE 8). The double mutant in 2603 Δ 80, Δ 104 double mutant was constructed by sequential allelic exchanges of the shown alleles.

Immunization protocol

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Immune sera for FACS experiments were obtained as follows.

Groups of 4 CD-1 outbred female mice 6-7 weeks old (Charles River Laboratories, Calco Italy) were immunized with the selected GBS antigens, (20 µg of each recombinant GBS antigen), suspended in 100 µl of PBS. Each group received 3 doses at days 0, 21 and 35. Immunization was performed through intra-peritoneal injection of the protein with an equal volume of Complete Freund's Adjuvant (CFA) for the first dose and Incomplete Freund's Adjuvant (IFA) for the following two doses. In each immunization scheme negative and positive control groups are used. Immune response was monitored by using serum samples taken on day 0 and 49.

FACS analysis

Preparation of paraformaldehyde treated GBS cells and their FACS analysis were carried out as follows.

GBS serotype COH1 strain cells were grown in Todd Hewitt Broth (THB; Difco Laboratories, Detroit, Mich.) to OD600nm = 0.5. The culture was centrifuged for 20 minutes at 5000 rpm and bacteria were washed once with PBS, resuspended in PBS containing 0.05% paraformaldehyde, and incubated for 1 hours at 37 °C and then overnight at 4°C. 50µl of fixed bacteria (OD600 0.1) were washed once with PBS, resuspended in 20µl of Newborn Calf Serum, (Sigma) and incubated for 20 min. at room temperature. The cells were then incubated for 1 hour at 4°C in 100µl of preimmune or immune sera, diluted 1:200 in dilution buffer (PBS, 20% Newborn Calf Serum, 0.1% BSA). After centrifugation and washing with 200µl of washing buffer (0.1% BSA in PBS), samples were incubated for 1 hour at 4°C with 50µl of R-Phicoerytrin conjugated F(ab)2 goat anti-mouse IgG (Jackson ImmunoResearch Laboratories; Inc.), diluted 1:100 in dilution buffer. Cells were washed with 200µl of washing buffer and resuspended in 200µl of PBS. Samples were analysed using a FACS Calibur apparatus (Becton Dickinson, Mountain View, Calf.) and data were analyzed using the Cell Quest Software (Becton Dickinson). A shift in mean fluorescence intensity of > 75 channels compared to preimmune sera from the same mice was considered positive. This cutoff

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Was determined from the mean plus two standard deviations of shifts obtained with control sera raised against mock purified recombinant proteins from cultures of *E. coli* carrying the empty expression vector and included in every experiment. Artifacts due to bacterial lysis were excluded using antisera raised against 6 different known cytoplasmic proteins all of which were negative

FACS data on COH1 single KO mutants for GBS 104 and GBS 80 indicated that GBS 80 is required for surface localization of GBS 104.

As shown in FIGURE 8, GBS 104 is not surface exposed in the Δ80 strain (second column, bottom), but is present in the whole protein extracts (see FIGURE 10). Mean shift values suggest that GBS 104 is partially responsible for GBS 80 surface exposure (Mean shift of GBS 80 is reduced to ~60% wild-type levels in Δ104), and that GBS 80 is over-expressed in the complemented strain (mean shift value ~200% wild-type level). The Δ80/pGBS 80 strain contains the GBS 80 orf cloned in the shuttle-vector pAM401 (Wirth, R., F. Y. An, et al. (1986). J Bacteriol 165(3): 831-6). The vector alone does not alter the secretion pattern of GBS 104 (right column). FACS was performed on midlog fixed bacteria with mouse polyclonal antibodies as indicated at left. Black peak is pre-immune sera, colored peaks are sera from immunized animals.

EXAMPLE 3: Deletion of GBS 80 causes attenuation in vivo.

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This example demonstrates that deletion of GBS 80 causes attenuation *in vivo*, suggesting that this protein contributes to bacterial virulence.

By using a mouse animal model, we studied the role of GBS 80 and GBS 104 in the virulence of S. agalactiae.

Groups of ten outbred female mice 5-6 week weeks old (Charles River Laboratories, Calco Italy) were inoculated intraperitoneally with different dilutions of the mutant strains and LD50 (lethal dose 50) were calculated according to the method of Reed and Muench [Reed, L. J. and H. Muench (1938). The American Journal of Hygiene 27(3): 493-7]. As presented in the table below the number of colony forming units (cfu) counted for both the $\Delta 80$ and the $\Delta 80$, $\Delta 104$ double mutants is about 10 fold higher when compared to the wild type strain suggesting that inactivation of GBS 80 but not GBS 104 is responsible for an attenuation in virulence. This finding indicates that GBS 80 gene in the AI-1 might contribute to virulence.

Table Lethal dose 50% analysis of AI-1 mutants in the 2603 strain background. LD50s were performed by IP injection of female CD1 mice at an age of 5-6 weeks. LD50s were calculated by the method of Reed and Muench (8).

GBS strain	LD ₅₀ , cfu	Number of Experiments
Wild Type 2603	2×10^{8}	4
Δ104 mutant	$\sim 2 \times 10^{8}$	1
Δ80 mutant	2.6×10^9	3
$\Delta 80$, $\Delta 104$ double mutant	$\sim 2 \times 10^9$	

EXAMPLE 4: Effect of Adhesin Island Sortase Deletions on Surface Antigen Presentation

This example demonstrates the effect of adhesin island sortase deletions on surface antigen presentation.

FACS analysis results set forth in FIGURE 9 show that a deletion in sortase SAG0648 prevented GBS 104 from reaching the surface and slightly reduced the surface exposure of GBS 80 (fourth panel; mean shift value ~60% wild-type COH1). In the double sortase knock-out strain, neither antigen was surface exposed (far right panel). Either sortase alone was sufficient for GBS 80 to arrive at the bacterial surface (third and fourth columns, top). No effect was seen on surface exposure of antigens GBS 80 or GBS 104 in the Δ GBS 52 strain. Antibodies derived from purified GBS 52 were either non-specific or were FACS negative for GBS 52 (data not shown). FACS analysis was performed as described above (see EXAMPLE 2).

As shown in FIGURE 10, inactivation of GBS 80 has no effect on GBS 104 expression as much as GBS 104 knock out doesn't change the total amount GBS 80 expressed. The Western blot of whole protein extracts (strains noted above lanes) probed with anti-GBS 80 antisera is shown in panel A. Arrow indicates expected size of GBS 80 (60 kDa). GBS 80 antibodies recognize a doublet, the lower band is not present in $\triangle GBS$ 80 strains. Panel B shows a Western blot of whole protein extracts probed with anti-GBS 104 antisera. Arrow indicates expected size of GBS 104 (99.4 kDa). Protein extracts were prepared from the same bacterial cultures used for FACS (FIGURES 8 and 9). In conclusion, although GBS 104 does not arrive at the surface in the Δ80 strain by FACS (FIGURE 8, second column), it is present at approximately wild-type levels in the whole protein preps (B, second lane). Approximately 20 µg of each protein extract was loaded per lane.

Western-blot analysis

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Aliquots of total protein extract mixed with SDS loading buffer (1x: 60 mM TRIS-HCl pH 6.8, 5% w/v SDS, 10% v/v glycerin, 0.1% Bromophenol Blue, 100 mM DTT) and boiled 5 minutes at 95° C, were loaded on a 12.5% SDS-PAGE precast gel (Biorad). The gel is run using a SDS-PAGE running buffer containing 250 mM TRIS, 2.5 mM Glycine and 0.1 %SDS. The gel is electroblotted onto nitrocellulose membrane at 200 mA for 60 minutes. The membrane is blocked for 60 minutes with PBS/0.05 % Tween-20 (Sigma), 10% skimmed milk powder and incubated O/N at 4° C with PBS/0.05 % Tween 20, 1% skimmed milk powder, with the appropriate dilution of the sera. After washing twice with PBS/0.05 % Tween, the membrane is incubated for 2 hours with peroxidaseconjugated secondary anti-mouse antibody (Amersham) diluted 1:4000. The nitrocellulose is washed three times for 10 minutes with PBS/0.05 % Tween and once with PBS and thereafter developed by Opti-4CN Substrate Kit (Biorad).

Example 5: Binding of Adhesin Island proteins to epithelial cells and effect of Adhesin Island proteins on capacity of GBS to adhere to epithelial cells.

This example illustrates the binding of AI proteins to epithelial cells and the effect of AI proteins on the capacity of GBS to adhere to epithelial cells.

Applicants analysed whether recombinant AI surface proteins GBS 80 or GBS 104 would demonstrate binding to various epithelial cells in a FACS analysis. Applicants also analysed whether -252WO 2006/078318

deletion of AI surface proteins GBS 80 or GBS 104 would effect the capacity of GBS to adhere to and invade ME180 cervical epithelial cells.

As shown in Figure 28, deletion of GBS 80 sequence from GBS strain isolate 2603 (serotype V) did not affect the capacity of the mutated GBS to adhere to and invade ME180 cervical epithelial cells. Here ME180 cervical carcinoma epithelial cells were infected with wild type GBS 2603 or GBS 2603 Δ80 isogenic mutant. After two hours of infection, non-adherent bacteria were washed off and infection prolonged for a further two hours and four hours. In invasion experiments, after each time point, was followed by a two hour antibiotic treatment. Cells were then lysed with 1% saponin and lysates platedon TSA plates. As shown in Figure 28, there was little difference between the percent invasion or percent adhesion of wild type and mutant strains up to the four hour time point.

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Figure 30 repeats this experiment with both $\Delta 104$ and $\Delta 80$ mutants from a different strain isolate. Here, ME180 cervical carcinoma epithelial cells were infected with GBS strain isolate COH (serotype III) wild type or COH1 ΔGBS 104 or COH1 $\Delta 80$ isogenic mutant. After one hour of infection, non-adherent bacteria were washed off and the cells were lysed with 1% saponin. The lysates were plated on TSA plates. As shown in Figure 30, while there was little difference in the percent invasion, there was a significant decrease in the percent association of the $\Delta 104$ mutant compared to both the wild type and $\Delta 80$ mutant.

The affect of AI surface proteins on the ability of GBS to translocate through an epithelial monolayer was also analysed. As shown in Figure 31, a GBS 80 knockout mutant strain partially loses the ability to translocate through an epithelial monolayer. Here epithelial monolayers were inoculated with wildtype or knockout mutant in the apical chamber of a transwell system for two hours and then non-adherent bacteria were washed off. Infection was prolonged for a further two and four hours. Samples were taken from the media of the basolateral side and the number of colony forming unties measured. Transepithelial electrical resistance measured prior to and after infection gave comparable values, indicating the maintenance of the integrity of the monolayer. By the six hour time point, the $\Delta 80$ mutants demonstrated a reduced percent transcytosis.

A similar experiment was conducted with GBS 104 knock out mutants. Here, as shown in Figure 22, the $\Delta 104$ mutants also demonstrated a reduced percent transcytosis, indicating that the mutant strains translocate through an epithelial monolayer less efficiently than their isogenic wild type counterparts.

Applicants also studied the effect of AI proteins on the capacity of a GBS strain to invade J774 macrophage-like cells. Here, J774 cells were infected with GBS COH1 wild type or COH1 Δ GBS104 or COH1 Δ GBS80 isogenic mutants. After one hour of infection, non-adherent bacteria were washed off and intracellular bacteria were recovered at two, four and six hours post antibiotic treatment. At each time point, cells were lysed with 0.25% Triton X-100 and lysates plated on TSA plates. As shown in Figure 32, the Δ 104 mutant demonstrated a significantly reduced percent invasion compared to both the wild type and Δ 80 mutant.

Example 6: Hyperoligomeric structures comprising AI surface proteins GBS 80 and GBS 104.

This example illustrates hyperoligomeric structures comprising AI surface proteins GBS 80 and GBS 104. A GBS isolate COH1 (serotype III) was adapted to increase expression of GBS 80. Figure 34 presents a regular negative stain electron micrograph of this mutant; no pilus or hyperoligomeric structures are distinguishable on the surface of the bacteria. When the EM stain is based on anti-GBS 80 antibodies labelled with 10 or 20 nm gold particles, the presence of GBS 80 throughout the hyperoligomeric structure is clearly indicated (Figures 36, 37 and 38). EM staining against GBS 104 (anti-GBS 104 antibodies labelled with 10 nm gold particles) also reveals the presence of GBS 104 primarily on or near the surface of the bacteria or potentially associated with bacterial peptidoglycans (Figure 39). Analysis of this same strain (over-expressing GBS 80) with a combination of both anti-GBS 80 (using 20 nm gold particles) and anti-GBS 104 (using 10 nm gold particles) reveals the presence of GBS 104 on the surface and within the hyperoligomeric structures (see Figures 40 and 41).

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Example 7: GBS 80 is necessary for polymer formation and GBS 104 and sortase SAG0648 are necessary for efficient pili assembly

This example demonstrates that GBS 80 is necessary for formation of polymers and that GBS 104 and sortase SAG0648 are necessary for efficient pili assembly. GBS 80 and GBS 104 polymeric assembly was systematically analyzed in Coh1 strain single knock out mutants of each of the relevant coding genes in AI-1 (GBS 80, GBS 104, GBS 52, sag0647, and sag0648). Figure 41 provides Western blots of total protein extracts (strains noted above lanes) probed with either anti-GBS 80 (left panel) sera or anti-GBS 104 sera (right panel) for each of these Coh1 and Coh1 knock out strains. (Coh1, wild type Coh1; Δ80, Coh1 with GBS 80 knocked out; Δ104, Coh1 with GBS 104 knocked out; Δ52, Coh1 with GBS 52 knocked out; Δ647, Coh1 with SAG0647 knocked out; Δ648, Coh1 with SAG0648 knocked out, Δ647-8, Coh1 with SAG0647 and SAG0648 knocked out; Δ80/pGBS80, Coh1 with GBS 80 knocked out but complemented with a high copy number plasmid expressing GBS 80. Asterisks identify the monomer of GBS 80 and GBS 104.)

The smear of immunoreactive material observed in the wild type strain, along with its disappearance in $\Delta 80$ and $\Delta 104$ mutants, is consistent with the notion that such high molecular weight structures are composed of covalently linked (SDS-resistant) GBS 80 and GBS 104 subunits. The immunoblotting with both anti-GBS 80 (α -GBS 80) and anti-GBS 104 (α -GBS 104) revealed that deletion of sortase SAG0648 also interferes with the assembly of high molecular weight species, whereas the knock out mutant of the second sortase (SAG0647), even if somehow reduced, still maintains the ability to form polymeric structures.

Total extracts form GBS were prepared as follows. Bacteria were grown in 50 ml of Todd-Hewitt broth (Difco) to an OD_{600nm} of 0.5-0.6 and successively pelleted. After two washes in PBS the pellet was resuspended and incubated 3 hours at 37°C with mutanolisin. Cells were then lysed with at

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least three freezing-thawing cycles in dry ice and a 37°C bath. The lysate was then centrifuged to eliminate the cellular debris and the supernatant was quantified. Approximately 40 μg of each protein extract was separated on SDS-PAGE. The gel was then subjected to immunoblotting with mice antisera and detected with chemiluminescence.

Example 8: GBS 80 is polymerized by an AI-2 sortase

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This example illustrates that GBS 80 can be polymerized not only by AI-1 sortases, but also by AI-2 sortases. Figure 42 shows total cell extract immunoblots of GBS 515 strain, which lacks AI-1. The left panel, where an anti-GBS 67 sera was used, shows that GBS 67 from AI-2 is assembled into high-molecular weight-complexes, suggesting the formation of a second type of pilus. The same high molecular structure is observed when GBS 80 is highly expressed by reintroducing the gene within a plasmid (pGBS 80). By using anti-GBS 80 (right panel) sera on the same extracts, again it is observed that, with GBS 80 over expression (515/pGBS 80), a high-molecular weight structure is assembled. This implies that, in the absence of AI-1 sortases, AI-2 sortases (SAG1405 and SAG1406) can complement the lacking function, still being able to assemble GBS 80 in a pilus structure.

Example 9: Coh1 produces a high molecular weight molecule, the GBS 80 pilin

This example illustrates that Coh1 produces a high molecular weight molecule, greater than 1000 kDa, which is the GBS 80 pilin. Figure 43 provides silver-stained electrophoretic gels that show that Coh1 produces two macromolecules. One of these macromolecules disappears in the Coh1 GBS 80 knock out cells, but does not disappear in the Coh1 GBS 52 knock out mutant cells. The last two lanes on the right were loaded with 15 times the amount loaded in the other lanes. This was done in order to be able to count the bands. By doing this, a conservative size estimate of the top bands was calculated by starting at 240 kDa and considering each of 14 higher bands as the result of consecutive additions of a GBS 80 monomer.

Coh1, wild type Coh1; Δ80, Coh1 cells with GBS 80 knocked out; Δ52, Coh1 cells with GBS 52 knocked out; Δ80/pGBS 80, Coh1 cells with GBS 80 knocked out and complemented with a high copy number construct expressing GBS 80.

Example 10. GBS 52 is a minor component of the GBS pilus

This example illustrates that GBS 52 is present in the GBS pilus and is a minor component of the pilus. Figure 45 shows an immunoblot of total cell extracts from a GBS Coh1 strain and a GBS Coh1 strain knocked out for GBS 52 (Δ 52). The total cell extracts were immunoblotted anti-GBS 80 antisera (left) and anti-GBS 52 antisera (right). Immunoblotting was performed using a 3-8% Trisacetate polyacrylamide gel (Invitrogen) which provided excellent separation of large molecular weight proteins (see figure 41). When the gel was incubated with anti-GBS 80 sera, the bands from the Coh1 wild-type strain appeared shifted when compared to the Δ 52 mutant. This observation

indicated a different size of the pilus polymeric components in the two strains. When the same gel was stripped and incubated with anti-GBS 52 sera the high-molecular subunits in the Coh1 wild-type strain showed similar molecular size of those in the correspondent lane in the left panel. These findings confirmed that GBS 52 is indeed associated with GBS 80 macro-molecular structures but represents a minor component of the GBS pilus.

Example 11: Pilus structures are present in the supernatant of GBS bacterial cultures

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This example illustrates that the pilus structure assembled in Coh1 GBS is present in the supernatant of a bacterial cell culture. Figure 46 shows an immunoblot where the protein extract of the supernatant from cultures of different GBS mutant strains (117 = Coh1 GBS 80 knockout; 159= Coh1 GBS 104 knockout; 202= Coh1 GBS 52 knockout; 206= Coh1 GBS sag0647 knockout; 208= Coh1 GBS sag0648 knockout; 197= Coh1 GBS sag0647/sag0648 knockout; 179= Coh1 GBS 80 knockout complemented with a high copy plasmid expressing GBS 80). GBS 80 antisera detects the presence of pilus structures in the appropriate Coh1 strains.

The protein extract was prepared as follows. Bacteria were grown in THB to an OD_{600nun} of 0.5-0.6 and the supernatant was separated from the cells by centrifugation. The supernatant was then filtered (Ø 0.2 μm) and 1 ml was added with 60% TCA for protein precipitation.

GBS pili were also extracted from the fraction of surface-exposed proteins in Coh1 strain and its GBS 80 knock out mutant as described hereafter. Bacteria were grown to an OD_{600nm} of 0.6 in 50 ml of THB at 37°C. Cells were washed once with PBS and the pellet was then resuspended in 0.1 M KPO4 pH 6.2, 40% sucrose, 10 mM MgCl2, 400U/ml mutanolysin and incubated 3 hours at 37°C. Protoplasts were separated by centrifugation and the supernatant was recovered and its protein content measured.

In order to study the dynamics of pilus production during different growth phases, 1 ml supernatant of a culture at different OD_{600nm} was TCA precipitated and loaded onto a 3-8% SDS-PAGE as described before. Figure 47 shows the corresponding Western blot with GBS 80 anti-sera. The first group of lanes (left five sample lanes) refer to a Coh1 strain growth (OD_{600nm} are noted above the lanes) whereas the second group of lanes (right five samples) are from a GBS 80 knock out strain over expressing GBS 80. The experiment shows that pilus macromolecular structures can be found in the supernatant in all of the growth phases tested.

Example 12: In GBS strain Coh1, only GBS 80 and a sortase (sag0647 or sag0648) is required for polymerization

This example describes requirements for pilus formation in Coh1. Figure 48 shows a Western blot of total protein extracts (prepared as described before) using anti-GBS 80 sera on Coh1 clones. (Coh1, wild type Coh1; Δ 104, Coh1 knocked out for GBS 104, Δ 647, Coh1 knocked out for sag0647, Δ 648, Coh1 knocked for sag0648, Δ 647-8, Coh1 knocked out for sag0647 and sag0648; 515, wild

80.) The data show that only the double sortase mutant is unable to polymerize GBS 80 indicating that the 'conditio sine qua non' for pilus polymerization is the co-existence of GBS 80 with at least one sortase. This result leads to a reasonable assumption that SAG1405 and SAG1406 are responsible for polymerization in this strain.

Example 13: GBS 80 can be expressed in *L. lactis* under its own promoter and terminator sequences

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This example demonstrates that *L. lactis*, a non-pathogenic bacterium, can express GBS AI

polypeptides such as GBS 80. *L. lactis* M1363 (*J. Bacteriol. 154* (1983):1-9) was transformed with a construct encoding GBS 80. Briefly, the construct was prepared by cloning a DNA fragment containing the gene coding for GBS 80 under its own promoter and terminator sequences into plasmid pAM401 (a shuttle vector for *E. coli* and other Gram positive bacteria; *J. Bacteriol. 163* (1986):831-836). Total extracts of the transformed bacteria in log phase were separated on SDS-PAGE,

transferred to membranes, and incubated with antiserum against GBS 80. A polypeptide corresponding to the molecular weight of GBS 80 was detected in the lanes containing total extracts of *L. lactis* transformed with the GBS 80 construct. See Figures 133A and 133B, lanes 6 and 7. This same polypeptide was not detected in the lane containing total extracts of *L. lactis* not transformed with the GBS 80 construct, lane 9. This example shows that *L. lactis* can express GBS 80 under its own promoter and terminator.

Example 14: L. lactis modified to express GBS AI-1 under the GBS 80 promoter and terminator sequences expresses GBS 80 in polymeric structures

This example demonstrates the ability of *L. lactis* to express GBS AI-1 polypeptides and to incorporate at least some of the polypeptides into oligomers. *L. lactis* was transformed with a construct containing the genes encoding GBS AI-1 polypeptides. Briefly, the construct was prepared by cloning a DNA fragment containing the genes for GBS 80, GBS 52, SAG0647, SAG0648, and GBS 104 under the GBS 80 promoter and terminator sequences into construct pAM401. The construct was transformed into *L. lactis* M1363. Total extracts of log phase transformed bacteria were separated on reducing SDS-PAGE, transferred to membranes, and incubated with antiserum against GBS 80. A polypeptide with a molecular weight corresponding to the molecular weight of GBS 80 was detected in the lanes containing *L. lactis* transformed with the GBS AI-1 encoding construct. See Figure 134, lane 2. In addition, the same lane also showed immunoreactivity of polypeptides having higher molecular weights than the polypeptide having the molecular weight of GBS 80. These higher molecular weight polypeptides are likely oligomers of GBS 80. Oligomers of similar molecular

weights were also observed on a Western hot of the culture supernatant of the transformed L. lactis. See lane 4 of Figure 135. Thus, this example shows that L. lactis transformed to express GBS AI-1 can efficiently polymerize GBS 80 in the form of a pilus. This pilus structure can likely be purified from either the cell culture supernatant or cell extracts.

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Example 15: Cloning and Expression of S. pneumoniae Sp0462

This example describes the production of a clone encoding a Sp0462 polypeptide and expression of the clone. To produce a clone encoding Sp0462, the open reading frame encoding Sp0462 was amplified using primers that annealed within the full-length Sp0462 open reading frame sequence. Figure 150A provides a 893 amino acid sequence of Sp0462. The primers used to produce a clone encoding the Sp0462 polypeptide are shown in Figure 150B. These primers annealed to the nucleotide sequences encoding the amino acid residues indicated by underlining in Figure 150A. Amplification of the open reading frame encoding Sp0462 using these primers produced the amplicon shown at lane 2 of the agarose gel provided in Figure 160. The Sp0462 clone encodes amino acid residues 38-862 of the 893 amino acid residue Sp0462 protein; the italicized residues in Figure 150A were eliminated. Figure 151A provides a schematic depiction of the recombinant Sp0462 polypeptide. Figure 151B shows a schematic depiction of the full-length Sp0462 polypeptide. Both the recombinant Sp0462 encoded by the clone and the full-length Sp0462 protein have two collagen binding protein type B (Cna B) domains and a von Hillebrand factor A (vWA) domain. The cloned recombinant Sp0462 lacks the LPXTG motif present in the full-length Sp0462 protein. Western blot analysis for expression of the Sp0462 clone did not result in detection of polypeptides with serum obtained from S. pneumoniae-infected patients (Figure 152A) or GBS 80 antiserum (Figure 152B).

Example 16: Cloning and Expression of S. pneumoniae Sp0463

This example describes the production of a clone encoding a Sp0463 polypeptide and detection of recombinant Sp0463 polypeptide expressed from the clone. To produce a clone encoding Sp0463, the open reading frame encoding Sp0463 was amplified using primers that annealed within the full-length Sp0463 open reading frame sequence. Figure 153A provides a 665 amino acid sequence of Sp0463. The primers used to produce the clone encoding Sp0463 polypeptide are shown in Figure 153B. These primers annealed to the nucleotide sequences encoding the amino acid residues indicated by underlining in Figure 153A. Amplification of the open reading frame encoding Sp0463 using these primers produced the amplicon shown at lane 3 of the agarose gel provided in Figure 160. The Sp0463 clone encodes amino acid residues 23-627 of the 665 amino acid residue Sp0463 protein; the italicized residues in Figure 153A were eliminated. Figure 154A provides a schematic depiction of the recombinant Sp0463 polypeptide. Figure 154B shows a schematic depiction of the full-length Sp0463 polypeptide. Both the recombinant Sp0463 encoded by the clone and the full-length Sp0463 protein have a Cna B domain and an E box motif. The cloned recombinant

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Sp0463 lacks the IPXIC mout present in the full-length Sp0463 protein. Expression of the Sp0463 clone resulted in the detection of a 60 kD polypeptide, the expected molecular weight of the recombinant Sp0463 polypeptide, by Western blot analysis. See Figure 155.

Example 17: Cloning and Expression of S. pneumoniae Sp0464

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This example describes the production of a clone encoding a Sp0464 polypeptide and detection of recombinant Sp0464 polypeptide expressed from the clone. To produce a clone encoding Sp0464, the open reading frame encoding Sp0464 was amplified using primers that annealed either within the full-length Sp0464 open reading frame sequence. Figure 157A provides a 393 amino acid sequence of Sp0464. The primers used to produce a clone encoding the Sp0464 polypeptide are shown in Figure 157B. These primers annealed to the nucleotide sequences encoding the amino acid residues indicated by underlining in Figure 157A. Amplification of the open reading frame encoding Sp0464 using these primers produced the amplicon shown at lane 4 of the agarose gel provided in Figure 160. The Sp0464 clone encodes amino acid residues 19-356 of the 393 amino acid residue Sp0464 protein; the italicized residues in Figure 157A were eliminated. Figure 158A provides a schematic depiction of the recombinant Sp0464 polypeptide. Figure 158B shows a schematic depiction of the full-length Sp0464 polypeptide. Both the recombinant Sp0464 encoded by the clone and the full-length Sp0464 protein have two Cna B domains. The cloned recombinant Sp0464 lacks the LPXTG motif present in the full-length Sp0464 protein. Expression of the Sp0464 clone resulted in the detection of a 38 kD polypeptide, the expected molecular weight of the recombinant Sp0464 polypeptide, by Western blot analysis. See Figure 159.

Example 18: Intranasal Immunization of Mice with Recombinant L. lactis Expressing GBS 80 and Subsequent Challenge

This example describes a method of intranasally immunizing mice using L. lactis that express GBS 80. Intranasal immunization consisted of 3 doses at days 0, 14 and 28, each dose administered in three consecutive days. Each day, groups of 3 CD-1 outbred female mice 6-7 weeks old (Charles River Laboratories, Calco Italy) were immunized intranasally with 10^9 or 10^{10} CFU of the recombinant Lactococcus lactis suspended in 20 μ l of PBS. In each immunization scheme negative (wild-type L. lactis) and positive (recombinant GBS80) control groups were used. The immune response of the dams was monitored by using serum samples taken on day 0 and 49. The female mice were bred 2-7 days after the last immunization (at approximately t=36-37), and typically had a gestation period of 21 days. Within 48 hours of birth, the pups were challenged via I.P. with GBS in a dose approximately equal to an amount which would be sufficient to kill 90 % of immunized pups (as determined by empirical data gathered from PBS control groups). The GBS challenge dose is preferably administered in 50ml of THB medium. Preferably, the pup challenge takes place at 56 to 61 days after the first immunization. The challenge inocula were prepared starting from frozen

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Example 19: Subcutaneous Immunization of Mice with Recombinant L. lactis Expressing GBS 80 and Subsequent Challenge

This example describes a method of subcutaneous immunization mice using L. lactis that express GBS 80. Subcutaneous immunization consists of 3 doses at days 0, 14 and 28. Groups of 3 CD-1 outbred female mice 6-7 weeks old (Charles River Laboratories, Calco Italy) were injected subcutaneously with 10° or 1010 CFU of the recombinant Lactococcus lactis suspended in 100 μl of PBS. In each immunization scheme, negative (wild-type L. lactis) and positive (recombinant GBS80) control groups were used. The immune response of the dams was monitored by using serum samples taken on day 0 and 49. The female mice were bred 2-7 days after the last immunization (at approximately t=36-37), and typically had a gestation period of 21 days. Within 48 hours of birth, the pups were challenged via I.P. with GBS in a dose approximately equal to an amount which would be sufficient to kill 90 % of immunized pups (as determined by empirical data gathered from PBS control groups). The GBS challenge dose is preferably administered in 50ml of THB medium. Preferably, the pup challenge takes place at 56 to 61 days after the first immunization. The challenge inocula were prepared starting from frozen cultures diluted to the appropriate concentration with THB prior to use. Survival of pups was monitored for 5 days after challenge.

Example 20: Immunization of Mice with GAS AI polypeptides and Subsequent Intranasal Challenge

This example describes a method of immunizing mice with GAS AI polypeptides and subsequently intranasally challenging the mice with GAS bacteria. Groups of 10 CD1 female mice aged between 6 and 7 weeks are immunized with a combination of GAS antigens of the invention GAS 15, GAS 16, and GAS 18, (15 µg of each recombinant antigen, derived from M1 strain SF370) or L. lactis expressing the M1 strain SF370 adhesin island, suspended in 100 µl of suitable solution. Each group receives 3 doses at days 0, 21 and 45. Immunization is performed through subcutaneous or intraperitoneal injection for the GAS 15, GAS 16, GAS 18 protein combination. The protein combination is administered with an equal volume of Complete Freund's Adjuvant (CFA) for the first dose and Incomplete Freund's Adjuvant (IFA) for the following two doses. Immunization is performed intranasally for the L. lactis expressing the M1 strain SF370 adhesin island. In each immunization scheme negative and positive control groups are used.

The negative control group for the mice immunized with the GAS 15, GAS 16, GAS 18 protein combination included mice immunized with PBS. The negative control group for the mice immunized with L. lactis expressing the M1 strain SF370 adhesin island, included mice immunized

with either wildtype in actis or In the mansformed with the pAM401 expression vector lacking any cloned adhesin island sequence.

The positive control groups included mice immunized with purified M1 strain SF370 M protein.

Immunized mice are then anaesthetized with Zoletil and challenged intranasally with a 25 μ L suspension containing 1.2 x 10⁶ or 1.2 x 10⁸ CFU of ISS 3348 in THB. Animals are observed daily and checked for survival.

Example 21: Active Maternal Immunization Assay

As used herein, an Active Maternal Immunization assay refers to an *in vivo* protection assay where female mice are immunized with the test antigen composition. The female mice are then bred and their pups are challenged with a lethal dose of GBS. Serum titers of the female mice during the immunization schedule are measured as well as the survival time of the pups after challenge.

Mouse immunization

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Specifically, groups of 4 CD-1 outbred female mice 6-8 weeks old (Charles River Laboratories, Calco Italy) are immunized with one or more GBS antigens, (20 µg of each recombinant GBS antigen), suspended in 100 µl of PBS. Each group receives 3 doses at days 0, 21 and 35. Immunization is performed through intra-peritoneal injection of the protein with an equal volume of Complete Freund's Adjuvant (CFA) for the first dose and Incomplete Freund's Adjuvant (IFA) for the following two doses. In each immunization scheme negative and positive control groups are used.

Immune response is monitored by using serum samples taken on day 0 and 49. The sera are analyzed as pools from each group of mice.

25 Active maternal immunization

A maternal immunization/neonatal pup challenge model of GBS infection was used to verify the protective efficacy of the antigens in mice. The mouse protection study was adapted from Rodewald et al. (Rodewald et al. J. Infect. Diseases 166, 635 (1992)). In brief, CD-1 female mice (6-8 weeks old) were immunized before breeding, as described above. The mice received 20 µg of protein per dose when immunized with a single antigen and 60 µg of protein per dose (15 µg of each antigen) when immunized with the combination of antigens. Mice were bred 2-7 days after the last immunization. Within 48 h of birth, pups were injected intraperitoneally with 50 µl of GBS culture. Challenge inocula were prepared starting from frozen cultures diluted to the appropriate concentration with THB before use. In preliminary experiments (not shown), the challenge doses per pup for each strain tested were determined to cause 90% lethality. Survival of pups was monitored for 2 days after challenge. Protection was calculated as (percentage

dead Control minus percentage dead Vaccine) divided by percentage dead Control multiplied by 100. Data were evaluated for statistical significance by Fisher's exact test.

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WO 2006/078318 PCT/US2005/027239

The invention encompasses, but is not limited to, the embodiments enumerated below.

- 1. An immunogenic composition comprising a purified Group B Streptococcus (GBS) adhesin island (AI) polypeptide in oligomeric form.
- 2. The immunogenic composition of embodiment 1 wherein the GBS AI polypeptide is selected from a GBS AI-1.
- 3. The immunogenic composition of embodiment 1 wherein the GBS AI polypeptide is selected from a GBS AI-2.
- 1. An immunogenic composition comprising a purified Group B Streptococcus (GBS) adhesin island (AI) polypeptide in oligomeric form.
- 2. The immunogenic composition of embodiment 1 wherein the GBS AI polypeptide is selected from a GBS AI-1.
- 3. The immunogenic composition of embodiment 1 wherein the GBS AI polypeptide is selected from a GBS AI-2.
- 4. The immunogenic composition of any of embodiments 1-3 wherein the GBS AI polypeptide comprises a sortase substrate motif.
- 5. The immunogenic composition of embodiment 4 wherein the sortase substrate motif is an LPXTG motif.
- 6. The immunogenic composition of embodiment 5 wherein the LPXTG motif is represented by the amino acid sequence XPXTG, wherein the X at amino acid position 1 is an L, an I, or an F and the X at amino acid position 3 is any amino acid residue.
 - 7. The immunogenic composition of any one of embodiments 1-3 wherein the GBS AI polypeptide affects the ability of GBS bacteria to adhere to epithelial cells.
- 8. The immunogenic composition of any one of embodiments 1-3 wherein the GBS AI polypeptide affects the ability of GBS bacteria to invade epithelial cells.
- 9. The immunogenic composition of any one of embodiments 1-3 wherein the GBS AI polypeptide affects the ability of GBS bacteria to translocate through an epithelial cell layer.
- 10. The immunogenic composition of any one of embodiments 1-3 wherein the GBS AI polypeptide is capable of associating with an epithelial cell surface.
- 30 11. The immunogenic composition of embodiment 10 wherein the associating with an epithelial cell surface is binding to the epithelial cell surface.
 - 12. The immunogenic composition of any of embodiments 1-3 wherein the GBS AI polypeptide is a full-length GBS AI protein.
 - 13. The immunogenic composition of any of embodiments 1-3 wherein the GBS AI polypeptide is a fragment of a full-length GBS AI protein.
 - 14. The immunogenic composition of embodiment 13 wherein the fragment comprises at least 7 contiguous amino acid residues of the GBS AI protein.

The immunogenic composition of embodiment 2 wherein the GBS AI polypeptide is selected from the group consisting of GBS 80, GBS 104, GBS 52, and fragments thereof.

16. The immunogenic composition of embodiment 3 wherein the GBS AI polypeptide is selected from the group consisting of GBS 59, GBS 67, GBS 150, 01521, 01523, 01524, and fragments thereof.

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- 17. The immunogenic composition of embodiment 15 wherein the GBS AI polypeptide is GBS 80.
- 18. The immunogenic composition of any of embodiments 1-3 or 15-17 wherein the oligomeric form is a hyperoligomer.
- 19. The immunogenic composition of any of embodiments 1-3, or 15-17 further comprising a Gram positive bacterium antigen not associated with an AI.
- 20. The immunogenic composition of embodiment 19 wherein the antigen is selected from the group consisting of GBS 322 and GBS 276.
 - 21. The immunogenic composition of embodiment 20 wherein the antigen is GBS 322.
- 22. An immunogenic composition comprising a purified Gram positive bacteria adhesin island (AI) polypeptide in an oligomeric form.
 - 23. The immunogenic composition of embodiment 22 wherein the Gram positive bacteria is of a genus selected from the group consisting of *Streptococcus*, *Enterococcus*, *Staphylococcus*, or *Listeria*.
- 24. The immunogenic composition of embodiment 23 wherein the Gram positive bacteria is of the genus *Streptococcus*.
 - 25. The immunogenic composition of any of embodiments 22-24 wherein the Gram positive bacteria AI polypeptide comprises a sortase substrate motif.
 - 26. The immunogenic composition of embodiment 25 wherein the sortase substrate motif is an LPXTG motif.
 - 27. The immunogenic composition of any one of embodiments 22-24 wherein the Gram positive bacteria AI polypeptide affects the ability of Gram positive bacteria to adhere to epithelial cells.
 - 28. The immunogenic composition of any one of embodiments 22-24 wherein the Gram positive bacteria AI polypeptide affects the ability of Gram positive bacteria to invade epithelial cells.
 - 29. The immunogenic composition of any one of embodiments 22-24 wherein the Gram positive bacteria AI polypeptide affects the ability of Gram positive bacteria to translocate through an epithelial cell layer.
 - 30. The immunogenic composition of any one of embodiments 22-24 wherein the Gram positive bacteria AI polypeptide is capable of associating with an epithelial cell surface.
 - 31. The immunogenic composition of embodiment 30 wherein the associating with an epithelial cell surface is binding to the epithelial cell surface.

32. The immunogenic composition of any of embodiments 22-24 wherein the Gram positive bacteria AI polypeptide is a full-length Gram positive bacteria AI protein.

- 33. The immunogenic composition of any of embodiments 22-24 wherein the Gram positive bacteria AI polypeptide is a fragment of a full-length Gram positive bacteria AI protein.
- 34. The immunogenic composition of embodiment 33 wherein the fragment comprises at least 7 contiguous amino acid residues of the Gram positive bacteria AI protein.

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- 35. The immunogenic composition of embodiment 24 wherein the genus *Streptococcus* bacteria is Group A Streptococcus (GAS) bacteria and the Gram positive bacteria AI polypeptide is a GAS AI polypeptide.
- 36. The immunogenic composition of embodiment 35 wherein the GAS AI polypeptide is selected from a GAS AI-1.
 - 37. The immunogenic composition of embodiment 35 wherein the GAS AI polypeptide is selected from a GAS AI-2.
 - 38. The immunogenic composition of embodiment 35 wherein the GAS AI polypeptide is selected from a GAS AI-3.
 - 39. The immunogenic composition of embodiment 35 wherein the GAS AI polypeptide is selected from a GAS AI-4.
 - 40. The immunogenic composition of any of embodiments 35-39 wherein the GAS AI polypeptide comprises a sortase substrate motif.
- 41. The immunogenic composition of embodiment 40 wherein the sortase substrate motif is an LPXTG motif.
 - 42. The immunogenic composition of embodiment 41 wherein the LPXTG motif is represented by XXXXG, wherein the X at the first amino acid position is an L, a V, an E, or a Q, wherein the X at the second amino acid position is P if the X at the first amino acid position is an L, the X at the second amino acid position is a V if the X at the first amino acid position is an E or a Q, or the X at the second amino acid position is a V or a P if the X at the first amino acid position is a V, wherein the X at the third amino acid position is any amino acid residue, and wherein the X at the fourth amino acid position is a T if the X at the first amino acid position is a V, an E, or a Q, or the X at the fourth amino acid position is a T, an S, or an A if the X at the first amino acid position is an L.
 - 43. The immunogenic composition of any one of embodiments 35-39 wherein the GAS AI polypeptide affects the ability of GAS bacteria to adhere to epithelial cells.
 - 44. The immunogenic composition of any one of embodiments 35-39 wherein the GAS AI polypeptide affects the ability of GAS bacteria to invade epithelial cells.
 - 45. The immunogenic composition of any one of embodiments 35-39 wherein the GAS AI polypeptide affects the ability of GAS bacteria to translocate through an epithelial cell layer.
 - 46. The immunogenic composition of any one of embodiments 35-39 wherein the GAS AI polypeptide is capable of associating with an epithelial cell surface.

The immunogenic composition of embodiment 46 wherein the associating with an epithelial cell surface is binding to the epithelial cell surface.

- 48. The immunogenic composition of any of embodiments 35-39 wherein the GAS AI polypeptide is a full-length GAS AI protein.
- 49. The immunogenic composition of any of embodiments 35-39 wherein the GAS AI polypeptide is a fragment of a full-length GAS AI protein.

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- 50. The immunogenic composition of embodiment 49 wherein the fragment comprises at least 7 contiguous amino acid residues of the GAS AI protein.
- 51. The immunogenic composition of embodiment 36 wherein the GAS AI-1 polypeptide is selected from the group consisting of M6_Spy0157, M6_Spy0159, M6_Spy0160, CDC SS 410_fimbrial, ISS3650 fimbrial, DSM2071 fimbrial, and fragments thereof.
- 52. The immunogenic composition of embodiment 37 wherein the GAS AI-2 polypeptide is selected from the group consisting of GAS15, GAS16, GAS18, and fragments thereof.
- 53. The immunogenic composition of embodiment 38 wherein the GAS AI-3 polypeptide is selected from the group consisting of SpyM3_0098, SpyM3_0100, SpyM3_0102, SpyM3_0104, SPs0100, SPs0102, SPs0104, SPs0106, orf78, orf80, orf82, orf84, spyM18_0126, spyM18_0128, spyM18_0130, spyM18_0132, SpyoM01000156, SpyoM01000155, SpyoM01000154, SpyoM01000153, SpyoM01000152, SpyoM01000151, SpyoM01000150, SpyoM01000149, ISS3040 fimbrial, ISS3776 fimbrial, ISS4959 fimbrial, and fragments thereof.
- 53. The immunogenic composition of embodiment 39 wherein the GAS AI-4 polypeptide is selected from the group consisting of 19224134, 19224135, 19224137, 19224139, 19224141, 20010296_fimbrial, 20020069_fimbrial, CDC SS 635_fimbrial, ISS4883_fimbrial, ISS4538_fimbrial, and fragments thereof.
- 54. The immunogenic composition of embodiment 24 wherein the *Streptococcus* bacteria is *Streptococcus pneumoniae* and the Gram positive bacteria AI polypeptide is a *S. pneumoniae* AI polypeptide.
- 55. The immunogenic composition of embodiment 54 wherein the *S. pneumoniae* AI polypeptide comprises a sortase substrate motif.
- 56. The immunogenic composition of embodiment 55 wherein the sortase substrate motif is an LPXTG motif.
 - 57. The immunogenic composition of embodiment 54 wherein the S. pneumoniae AI polypeptide affects the ability of S. pneumoniae to adhere to epithelial cells.
 - 58. The immunogenic composition of embodiment 54 wherein the S. pneumoniae AI polypeptide affects the ability of S. pneumoniae to invade epithelial cells.
 - 59. The immunogenic composition of embodiment 54 wherein the S. pneumoniae AI polypeptide affects the ability of S. pneumoniae to translocate through an epithelial cell layer.
 - 60. The immunogenic composition of embodiment 54 wherein the *S. pneumoniae* AI polypeptide is capable of associating with an epithelial cell surface.

epithelial cell surface is binding to the epithelial cell surface.

- 62. The immunogenic composition of embodiment 54 wherein the *S. pneumoniae* AI polypeptide is a full-length *S. pneumoniae* AI protein.
- 63. The immunogenic composition of embodiment 54 wherein the *S. pneumoniae* AI polypeptide is a fragment of a full-length *S. pneumoniae* AI protein.

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- 64. The immunogenic composition of embodiment 63 wherein the fragment comprises at least 7 contiguous amino acid residues of the *S. pneumoniae* AI protein.
- 65. The immunogenic composition of embodiment 54 wherein the *S. pneumoniae* AI polypeptide is selected from the group consisting of SP0462, SP0463, SP0464, orf3_670, orf4_670, orf5_670, ORF3_14CSR, ORF4_14CSR, ORF5_14CSR, ORF3_19AH, ORF4_19AH, ORF5_19AH, ORF3_19FTW, ORF4_19FTW, ORF5_19FTW, ORF3_23FP, ORF4_23FP, ORF5_23FP, ORF3_23FTW, ORF4_23FTW, ORF5_23FTW, ORF3_6BF, ORF4_6BF, ORF5_6BF, ORF3_6BSP, ORF4_6BSP, ORF5_6BSP, ORF5_
 - 66. The immunogenic composition of any one of embodiments 22-24, 35-39, 51-54, or 65 wherein the oligomeric form is a hyperoligomer.
 - 67. The immunogenic composition of any one of embodiments 22-24, 35-39, 51-54, or 65 further comprising a Gram positive bacteria antigen not associated with an AI.
- 68. The immunogenic composition of embodiment 67 wherein the antigen is selected from the group consisting of GBS 322 and GBS 276.
 - 69. An immunogenic composition comprising a first and a second Group B Streptococcus (GBS) adhesin island (AI) polypeptide.
 - 70. The immunogenic composition of embodiment 69 wherein a full-length polynucleotide sequence encoding for the first GBS AI polypeptide is not present in a GBS bacteria genome comprising a polynucleotide sequence encoding for the second GBS AI polypeptide.
 - 71. The immunogenic composition of embodiment 69 wherein polynucleotides encoding the first and the second GBS AI polypeptide are each present in genomes of more than one GBS serotype and strain isolate.
- 72. The immunogenic composition of embodiment 69 wherein the first GBS AI polypeptide 30 is encoded by a GBS AI-1.
 - 73. The immunogenic composition of embodiment 69 wherein the first GBS AI polypeptide is encoded by a GBS AI-2.
 - 74. The immunogenic composition of embodiment 72 wherein the second GBS AI polypeptide is encoded by a GBS AI-2.
- 35 , 75. The immunogenic composition of embodiment 73 wherein the second GBS AI polypeptide is encoded by a GBS AI-2.
 - 76. The immunogenic composition of embodiment 72 wherein the second GBS AI polypeptide is encoded by a GBS AI-1.

polypeptide is encoded by a GBS AI-1.

- 78. The immunogenic composition of embodiment 72 wherein the first GBS AI polypeptide is selected from the group consisting of GBS 80, GBS 104, GBS 52, and fragments thereof.
- 79. The immunogenic composition of embodiment 73 wherein the first GBS AI polypeptide is selected from the group consisting of GBS 59, GBS 67, GBS 150, 01521, 01523, 01524, and fragments thereof.

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- 80. The immunogenic composition of embodiment 74 or 75 wherein the second GBS AI polypeptide is selected from the group consisting of GBS 59, GBS 67, GBS 150, 01521, 01523, 01524, and fragments thereof, and wherein the first and the second GBS AI polypeptide are not the same polypeptide.
- 81. The immunogenic composition of embodiment 76 or 77 wherein the second GBS AI polypeptide is selected from the group consisting of GBS 80, GBS 104, GBS 52, and fragments thereof, and wherein the first and the second GBS AI polypeptide are not the same polypeptide.
- 82. The immunogenic composition of any one of embodiments 69-77 wherein the first GBS AI polypeptide comprises a sortase substrate motif.
- 83. The immunogenic composition of embodiment 82 wherein the sortase substrate motif is an LPXTG motif.
- 84. The immunogenic composition of embodiment 83 wherein the LPXTG motif is represented by the sequence XPXTG, wherein the X at amino acid position 1 is an L, an I, or an F and the X at amino acid position 3 is any amino acid residue.
- 85. The immunogenic composition of any one of embodiments 69-77 wherein the first GBS AI polypeptide affects the ability of GBS bacteria to adhere to epithelial cells.
- 86. The immunogenic composition of any one of embodiments 69-77 wherein the first GBS AI polypeptide affects the ability of GBS bacteria to invade epithelial cells.
- 87. The immunogenic composition of any one of embodiments 69-77 wherein the first GBS AI polypeptide affects the ability of GBS bacteria to translocate through an epithelial cell layer.
- 88. The immunogenic composition of any one of embodiments 69-77 wherein the first GBS AI polypeptide is capable of associating with an epithelial cell surface.
- 89. The immunogenic composition of embodiment 88 wherein the associating with an epithelial cell surface is binding to the epithelial cell surface.
- 90. The immunogenic composition of any of embodiments 69-77 wherein the first GBS AI polypeptide is a full-length GBS AI protein.
- 91. The immunogenic composition of any of embodiments 69-77 wherein the first GBS AI polypeptide is a fragment of a full-length GBS AI protein.
 - 92. The immunogenic composition of embodiment 91 wherein the fragment comprises at least 7 contiguous amino acid residues of the first GBS AI protein.

AI polypeptide is in oligomeric form.

- 94. The immunogenic composition of any one of embodiments 69-77 wherein the second GBS AI polypeptide is in oligomeric form.
- 95. The immunogenic composition of any one of embodiments 69-79 wherein the first and the second GBS AI polypeptide are associated in a single oligomeric form.

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- 96. The immunogenic composition of embodiment 95 wherein the first and the second GBS AI polypeptides are chemically associated.
- 97. The immunogenic composition of embodiment 95 wherein the first and the second GBS10 AI polypeptides are physically associated.
 - 98. The immunogenic composition of embodiment 93 wherein the oligomeric form is a hyperoligomer.
 - 99. The immunogenic composition of embodiment 94 wherein the oligomeric form is a hyperoligomer.
- 15 100. The immunogenic composition of embodiment 76 wherein the first GBS AI polypeptide is GBS 80 and the second GBS AI polypeptide is GBS 104.
 - 101. The immunogenic composition of embodiment 74 wherein the first GBS AI polypeptide is GBS 80 and the second GBS AI polypeptide is GBS 67.
 - 102. The immunogenic composition of any one of embodiments 69-79, 100, or 101 further comprising a GBS polypeptide not associated with an AI.
 - 103. The immunogenic composition of embodiment 102 wherein the GBS polypeptide not associated with an AI is selected from the group consisting of GBS 322 and GBS 276.
 - 104. The immunogenic composition of embodiment 103 wherein the GBS polypeptide not associated with an AI is GBS 322.
- 25 105. An immunogenic composition comprising a first and a second Gram positive bacteria adhesin island (AI) polypeptide.
 - 106. The immunogenic composition of embodiment 105 wherein a full length polynucleotide sequence encoding for the first Gram positive bacteria AI polypeptide is not present in a genome of a Gram positive bacteria comprising a full length polynucleotide sequence encoding for the second Gram positive bacteria AI polypeptide.
 - 107. The immunogenic composition of embodiment 105 wherein polynucleotides encoding the first and the second Gram positive bacteria AI polypeptide are each present in genomes of more than one Gram positive bacteria serotype and strain isolate.
- 108. The immunogenic composition of embodiment 105 wherein the first and the second 35 Gram positive bacteria AI polypeptides are of different Gram positive bacteria species.
 - 109. The immunogenic composition of embodiment 105 wherein the first and the second Gram positive bacteria AI polypeptides are of the same Gram positive bacteria species.

Gram positive bacteria AI polypeptides are from different AI subtypes.

111. The immunogenic composition of embodiment 105 wherein the first and the second Gram positive bacteria AI polypeptides are from the same AI subtype.

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- 112. The immunogenic composition of embodiment 105 wherein the first Gram positive bacteria AI polypeptide has detectable surface exposure on a first Gram positive bacteria strain or serotype but not a second Gram positive bacteria strain or subtype and the second Gram positive bacteria AI polypeptide has detectable surface exposure on the second Gram positive bacteria strain or serotype but not the first Gram positive bacteria strain or serotype.
- 113. The immunogenic composition of embodiment 105 wherein the Gram positive bacteria is S. pneumonaie, S. mutans, E. faecalis, E. faecium, C. difficile, L. monocytogenes, or C. diphtheriae.
- 114. The immunogenic composition of any of embodiments 105-113 wherein the first and the second Gram positive bacteria AI polypeptides comprise a sortase substrate motif.
- 115. The immunogenic composition of embodiment 114 wherein the sortase substrate motif is an LPXTG motif.
 - 116. The immunogenic composition of embodiment 115 wherein the LPXTG motif is represented by XXXXG, wherein the X at amino acid position 1 is an L, a V, an E, an I, an F, or a Q, wherein X at amino acid position 2 is a P if X at amino acid position 1 is an L, an I, or an F, wherein X at amino acid position 2 is a V if X at amino acid position 1 is a E or a Q, wherein X at amino acid position 2 is a V or a P if X at amino acid position 1 is a V, wherein X at amino acid position 3 is any amino acid residue, wherein X at amino acid position 4 is a T if X at amino acid position 1 is a V, E, I, F, or Q, and wherein X at amino acid position 4 is a T, S, or A if X at amino acid position 1 is an L.
- 117. The immunogenic composition of embodiment 105 wherein the first Gram positive bacteria AI polypeptide is a first Group A Streptococcus (GAS) AI polypeptide.
- 118. The immunogenic composition of embodiment 117 wherein the first GAS AI polypeptide comprises a sortase substrate motif.
- 119. The immunogenic composition of embodiment 118 wherein the sortase substrate motif is an LPXTG motif.
- 120. The immunogenic composition of embodiment 119 wherein the LPXTG motif is represented by XXXXG, wherein the X at the first amino acid position is an L, a V, an E, or a Q, wherein the X at the second amino acid position is P if the X at the first amino acid position is an L, the X at the second amino acid position is a V if the X at the first amino acid position is an E or a Q, or the X at the second amino acid position is a V or a P if the X at the first amino acid position is a V, wherein the X at the third amino acid position is any amino acid residue, and wherein the X at the fourth amino acid position is a T if the X at the first amino acid position is a V, an E, or a Q, or the X at the fourth amino acid position is a T, an S, or an A if the X at the first amino acid position is an L.
- 121. The immunogenic composition of embodiment 117 wherein the first GAS AI polypeptide affects the ability of GAS bacteria to adhere to epithelial cells.

polypeptide affects the ability of GAS bacteria to invade epithelial cells.

- 123. The immunogenic composition of embodiment 117 wherein the first GAS AI polypeptide affects the ability of GAS bacteria to translocate through an epithelial cell layer.
- 124. The immunogenic composition of embodiment 117 wherein the first GAS AI polypeptide is capable of associating with an epithelial cell surface.

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- 125. The immunogenic composition of embodiment 117 wherein the associating with an epithelial cell surface is binding to the epithelial cell surface.
- 126. The immunogenic composition of embodiment 117 wherein the first GAS AI polypeptide is a full-length GAS AI protein.
 - 127. The immunogenic composition of embodiment 117 wherein the first GAS AI polypeptide is a fragment of a full-length GAS AI protein.
 - 128. The immunogenic composition of embodiment 127 wherein the fragment comprises at least 7 contiguous amino acid residues of the GAS AI protein.
- 15 129. The immunogenic composition of embodiment 117 wherein the first GAS AI polypeptide is a first GAS AI-1 polypeptide.
 - 130. The immunogenic composition of embodiment 117 wherein the first GAS AI polypeptide is a first GAS AI-2 polypeptide.
- 131. The immunogenic composition of embodiment 117 wherein the first GAS AI20 polypeptide is a first GAS AI-3 polypeptide.
 - 132. The immunogenic composition of embodiment 117 wherein the first GAS AI polypeptide is a first GAS AI-4 polypeptide.
 - 133. The immunogenic composition of any one of embodiments 117 or 129-132 wherein the second Gram positive bacteria AI polypeptide is a second GAS AI polypeptide.
 - 134. The immunogenic composition of embodiment 133 wherein the second GAS AI polypeptide is a second GAS AI-1 polypeptide.
 - 135. The immunogenic composition of embodiment 133 wherein the second GAS AI polypeptide is a second GAS AI-2 polypeptide.
- 136. The immunogenic composition of embodiment 133 wherein the second GAS AI 30 polypeptide is a second GAS AI-3 polypeptide.
 - 137. The immunogenic composition of embodiment 133 wherein the second GAS AI polypeptide is a second GAS AI-4 polypeptide.
 - 138. The immunogenic composition of embodiment 129 wherein the first GAS AI-1 polypeptide is selected from the group consisting of M6_Spy0157, M6_Spy0159, M6_Spy0160, CDC SS 410_fimbrial, ISS3650_fimbrial, DSM2071_fimbrial, and fragments thereof.
 - 139. The immunogenic composition of embodiment 130 wherein the first GAS AI-2 polypeptide is selected from the group consisting of GAS15, GAS16, GAS18, and fragments thereof.

polypeptide is selected from the group consisting of SpyM3_0098, SpyM3_0100, SpyM3_0102, SpyM3_0104, SPs0100, SPs0102, SPs0104, SPs0106, orf78, orf80, orf82, orf84, spyM18_0126, spyM18_0128, spyM18_0130, spyM18_0132, SpyoM01000156, SpyoM01000155, SpyoM01000154, SpyoM01000153, SpyoM01000152, SpyoM01000151, SpyoM01000150, SpyoM01000149, ISS3040_fimbrial, ISS3776_fimbrial, ISS4959_fimbrial, and fragments thereof.

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- 141. The immunogenic composition of embodiment 132 wherein the first GAS AI-4 polypeptide is selected from the group consisting of 19224134, 19224135, 19224137, 19224139, 19224141, 20010296_fimbrial, 20020069_fimbrial, CDC SS 635_fimbrial, ISS4883_fimbrial, ISS4538 fimbrial, and fragments thereof.
- 142. The immunogenic composition of embodiment 134 wherein the second GAS AI-1 polypeptide is selected from the group consisting of M6_Spy0157, M6_Spy0159, M6_Spy0160, CDC SS 410_fimbrial, ISS3650_fimbrial, DSM2071 fimbrial, and fragments thereof.
- 143. The immunogenic composition of embodiment 135 wherein the second GAS AI-2 polypeptide is selected from the group consisting of GAS15, GAS16, GAS18, and fragments thereof.
- 144. The immunogenic composition of embodiment 136 wherein the second GAS AI-3 polypeptide is selected from the group consisting of SpyM3_0098, SpyM3_0100, SpyM3_0102, SpyM3_0104, SPs0100, SPs0102, SPs0104, SPs0106, orf78, orf80, orf82, orf84, spyM18_0126, spyM18_0128, spyM18_0130, spyM18_0132, SpyoM01000156, SpyoM01000155, SpyoM01000154, SpyoM01000153, SpyoM01000152, SpyoM01000151, SpyoM01000150, SpyoM01000149, ISS3040_fimbrial, ISS3776_fimbrial, ISS4959_fimbrial, and fragments thereof.
- 145. The immunogenic composition of embodiment 137 wherein the second GAS AI-4 polypeptide is selected from the group consisting of 19224134, 19224135, 19224137, 19224139, 19224141, 20010296_fimbrial, 20020069_fimbrial, CDC SS 635_fimbrial, ISS4883_fimbrial, ISS4538 fimbrial, and fragments thereof.
- 146. The immunogenic composition of any one of embodiments 117-132 or 138-141 wherein the second Gram positive bacteria AI polypeptide is a Group B Streptococcus (GBS) AI polypeptide.
- 147. The immunogenic composition of embodiment 146 wherein the GBS AI polypeptide comprises a sortase substrate motif.
- 148. The immunogenic composition of embodiment 147 wherein the sortase substrate motif is an LPXTG motif.
- 149. The immunogenic composition of embodiment 148 wherein the LPXTG motif is represented by the amino acid sequence XPXTG, wherein the X at amino acid position 1 is an L, an I, or an F and the X at amino acid position 3 is any amino acid residue.
- 150. The immunogenic composition of embodiment 146 wherein the GBS AI polypeptide affects the ability of GBS bacteria to adhere to epithelial cells.
- 151. The immunogenic composition of embodiment 146 wherein the GBS AI polypeptide affects the ability of GBS bacteria to invade epithelial cells.

The immunogenic composition of embodiment 146 wherein the GBS AI polypeptide affects the ability of GBS bacteria to translocate through an epithelial cell layer.

- 153. The immunogenic composition of embodiment 146 wherein the GBS AI polypeptide is capable of associating with an epithelial cell surface.
- 154. The immunogenic composition of embodiment 146 wherein the associating with an epithelial cell surface is binding to the epithelial cell surface.

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- 155. The immunogenic composition of embodiment 146 wherein the GBS AI polypeptide is a full-length GBS AI protein.
- 156. The immunogenic composition of embodiment 146 wherein the GBS AI polypeptide is a fragment of a full-length GBS AI protein.
 - 157. The immunogenic composition of embodiment 156 wherein the fragment comprises at least 7 contiguous amino acid residues of the GBS AI protein.
 - 158. The immunogenic composition of embodiment 146 wherein the GBS AI polypeptide is a GBS AI-1 polypeptide.
 - 159. The immunogenic composition of embodiment 146 wherein the GBS AI polypeptide is a GBS AI-2 polypeptide.
 - 160. The immunogenic composition of embodiment 158 wherein the GBS AI-1 polypeptide is selected from the group consisting of GBS 80, GBS 104, GBS 52, and fragments thereof.
 - 161. The immunogenic composition of embodiment 159 wherein the GBS AI-2 polypeptide is selected from the group consisting of GBS 59, GBS 67, GBS 150, 01521, 01523, 01524, and fragments thereof.
 - 162. The immunogenic composition of any one of embodiments 117-132 or 138-141 wherein the second Gram positive bacteria AI polypeptide is a *Streptococcus pneumoniae* AI polypeptide.
 - 163. The immunogenic composition of embodiment 162 wherein the *S. pneumoniae* AI polypeptide comprises a sortase substrate motif.
 - 164. The immunogenic composition of embodiment 163 wherein the sortase substrate motif is an LPXTG motif.
 - 165. The immunogenic composition of embodiment 162 wherein the S. pneumoniae AI polypeptide affects the ability of S. pneumoniae to adhere to epithelial cells.
 - 166. The immunogenic composition of embodiment 162 S. pneumoniae AI polypeptide affects the ability of S. pneumoniae to invade epithelial cells.
 - 167. The immunogenic composition of embodiment 162 wherein the S. pneumoniae AI polypeptide affects the ability of S. pneumoniae to translocate through an epithelial cell layer.
 - 168. The immunogenic composition of embodiment 162 wherein the S. pneumoniae AI polypeptide is capable of associating with an epithelial cell surface.
 - 169. The immunogenic composition of embodiment 168 wherein the associating with an epithelial cell surface is binding to the epithelial cell surface.

polypeptide is a full-length S. pneumoniae AI protein.

- 171. The immunogenic composition of embodiment 162 wherein the S. pneumoniae AI polypeptide is a fragment of a full-length S. pneumoniae AI protein.
- 172. The immunogenic composition of embodiment 162 wherein the fragment comprises at least 7 contiguous amino acid residues of the *S. pneumoniae* AI protein.

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- 173. The immunogenic composition of embodiment 162 wherein the *S. pneumoniae* AI polypeptide is selected from the group consisting of SP0462, SP0463, SP0464, orf3_670, orf4_670, orf5_670, ORF3_14CSR, ORF4_14CSR, ORF5_14CSR, ORF3_19AH, ORF4_19AH, ORF5_19AH, ORF3_19FTW, ORF4_19FTW, ORF5_19FTW, ORF3_23FP, ORF4_23FP, ORF5_23FP, ORF3_23FTW, ORF4_23FTW, ORF5_23FTW, ORF3_6BF, ORF4_6BF, ORF5_6BF, ORF3_6BSP, ORF4_6BSP, ORF5_6BSP, ORF
- 174. The immunogenic composition of any one of embodiments 105-117 wherein the first Gram positive bacteria AI polypeptide is in oligomeric form.
- 175. The immunogenic composition of embodiment 174 wherein the oligomeric form is a hyperoligomer.
- 176. The immunogenic composition of embodiment 174 wherein the second Gram positive bacteria AI polypeptide is in oligomeric form.
- 177. The immunogenic composition of embodiment 176 wherein the oligomeric form is a hyperoligomer.
 - 178. The immunogenic composition of embodiment 176 wherein the first and the second Gram positive bacteria AI polypeptide are associated in a single oligomeric form.
 - 179. The immunogenic composition of embodiment 178 wherein the first and the second Gram positive bacteria AI polypeptide are chemically associated.
 - 180. The immunogenic composition of embodiment 178 wherein the first and the second Gram positive bacteria AI polypeptide are physically associated.
 - 181. The immunogenic composition of any one of embodiments 105-117 further comprising a Gram positive bacteria polypeptide not associated with an AI.
 - 182. The immunogenic composition of embodiment 181 wherein the Gram positive bacteria polypeptide not associated with an AI is selected from the group consisting of GBS 322 and GBS 276.
 - 183. The immunogenic composition of embodiment 182 wherein the Gram positive bacteria polypeptide not associated with an AI is GBS 322.
 - 184. A modified Gram positive bacterium adapted to produce increased levels of AI surface protein.
- 185. The modified Gram positive bacterium of embodiment 184 wherein the AI surface protein is in oligomeric form.
 - 186. The modified Gram positive bacterium of embodiment 185 wherein the oligomeric form is a hyperoligomer.

The modified Gram positive bacterium of any one of embodiments 184-186 which is a Group B Streptococcus bacterium.

- 188. The modified Gram positive bacterium of any one of embodiments 184-186 which is a Group A Streptococcus bacterium.
- 189. The modified Gram positive bacterium of any one of embodiments 184-186 which is a non-pathogenic Gram positive bacterium.

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- 190. The modified Gram positive bacterium of embodiment 189 wherein the non-pathogenic Gram positive bacterium is *Streptococus gordonii*.
- 191. The modified Gram positive bacterium of embodiment 189 wherein the non-pathogenic Gram positive bacterium is *Lactococcus lactis*.
 - 192. The modified Gram positive bacterium of any one of embodiments 184-186 which has been inactivated and wherein the AI surface protein is exposed on the surface of the Gram positive bacterium.
 - 193. The modified Gram positive bacterium of any one of embodiments 184-186 which has been attenuated and wherein the AI surface protein is exposed on the surface of the Gram positive bacterium.
 - 194. The modified GBS bacterium of embodiment 187 which has been inactivated and wherein the AI surface protein is exposed on the surface of the GBS bacterium.
 - 195. The modified GBS bacterium of embodiment 187 which has been attenuated and wherein the AI surface protein is exposed on the surface of the GBS bacterium.
 - 196. The modified GAS bacterium of embodiment 188 which has been inactivated and wherein the AI surface protein is exposed on the surface of the GAS bacterium.
 - 197. The modified GAS bacterium of embodiment 188 which has been attenuated and wherein the AI surface protein is exposed on the surface of the GAS bacterium.
 - 198. The modified non-pathogenic bacterium of embodiment 189 which has been inactivated and wherein the AI surface protein is exposed on the surface of the non-pathogenic Gram positive bacterium.
 - 199. The modified non-pathogenic bacterium of embodiment 189 which has been attenuated and wherein the AI surface protein is exposed on the surface of the non-pathogenic Gram positive bacterium.
 - 200. A method for manufacturing an oligomeric adhesin island (AI) surface antigen comprising:

culturing a Gram positive bacterium that expresses an oligomeric AI surface antigen and isolating the expressed oligomeric AI surface antigen.

- 201. The method of embodiment 200 wherein the step of isolating is performed by collecting said oligomeric AI surface antigen from Gram positive bacterium secretions in the Gram positive bacterium culture.
 - 202. The method of embodiment 200 further comprising a step of purifying.

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The method of embodiment 202 wherein the oligomeric AI surface antigen is purified from the Gram positive bacterium cell surface.

- 204. The method of embodiment 200 wherein the Gram positive bacterium is adapted for increased AI protein expression.
- 205. The method of any one of embodiments 200-204 wherein the Gram positive bacterium is a Group A Streptococcus bacterium.

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- 206. The method of any one of embodiments 200-204 wherein the Gram positive bacterium is a Group B Streptococcus bacterium.
- 207. The method of any one of embodiments 200-204 wherein the oligomeric AI surface antigen is in hyperoligomeric form.
 - 208. The method of embodiment 200 wherein the Gram positive bacterium expresses the oligomeric AI surface antigen recombinantly.
 - 209. The method of embodiment 208 wherein the Gram positive bacterium further manipulated expresses at least 1 AI sortase.
- 15 210. The modified Gram positive bacterium of any one of embodiments 184-186 which is a S. pneumoniae bacterium.
 - 211. The method of any one of embodiments 200-204 wherein the Gram positive bacterium is S. pneumoniae.

1. An immunogenic composition comprising a purified Group B Streptococcus (GBS) adhesin island (AI) polypeptide in oligomeric form.

2. The immunogenic composition of claim 1 wherein the GBS AI polypeptide is selected from a GBS AI-1.

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- 3. The immunogenic composition of claim 1 wherein the GBS AI polypeptide is selected from a GBS AI-2.
- 4. The immunogenic composition of claim 2 wherein the GBS AI polypeptide is selected from the group consisting of GBS 80, GBS 104, GBS 52, and fragments thereof.
- 5. The immunogenic composition of claim 3 wherein the GBS AI polypeptide is selected from the group consisting of GBS 59, GBS 67, GBS 150, 01521, 01523, 01524, and fragments thereof.
 - 6. The immunogenic composition of claim 4 wherein the GBS AI polypeptide is GBS 80.
- 7. The immunogenic composition of any of claims 1-6 wherein the oligomeric form is a hyperoligomer.
 - 8 (22). An immunogenic composition comprising a purified Gram positive bacteria adhesin island (AI) polypeptide in an oligomeric form.
 - 9 (23). The immunogenic composition of claim 8 wherein the Gram positive bacteria is of a genus selected from the group consisting of *Streptococcus*, *Enterococcus*, *Staphylococcus*, *Clostridium*, *Corynebacterium*, or *Listeria*.
 - 10 (24). The immunogenic composition of claim 9 wherein the Gram positive bacteria is of the genus *Streptococcus*.
 - 11 (35). The immunogenic composition of claim 10 wherein the genus *Streptococcus* bacteria is Group A Streptococcus (GAS) bacteria and the Gram positive bacteria AI polypeptide is a GAS AI polypeptide.
 - 12 (36). The immunogenic composition of claim 11 wherein the GAS AI polypeptide is selected from a GAS AI-1.
 - 13 (37). The immunogenic composition of claim 11 wherein the GAS AI polypeptide is selected from a GAS AI-2.
 - 14 (38). The immunogenic composition of claim 11 wherein the GAS AI polypeptide is selected from a GAS AI-3.
 - 15 (39). The immunogenic composition of claim 11 wherein the GAS AI polypeptide is selected from a GAS AI-4.
- 16 (66). The immunogenic composition of any one of claims 8-15 wherein the oligomeric form is a hyperoligomer.
 - 17. An immunogenic composition comprising a first and a second Group B Streptococcus (GBS) adhesin island (AI) polypeptide.

18. The immunogenic composition of claim 17 wherein the first GBS AI polypeptide is encoded by a GBS AI-1.

- 19. The immunogenic composition of claim 18 wherein the second GBS AI polypeptide is encoded by a GBS AI-2.
- 20. The immunogenic composition of claim 18 wherein the first GBS AI polypeptide is selected from the group consisting of GBS 80, GBS 104, GBS 52, and fragments thereof.

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- 21. The immunogenic composition of claim 19 wherein the second GBS AI polypeptide is selected from the group consisting of GBS 59, GBS 67, GBS 150, 01521, 01523, 01524, and fragments thereof, and wherein the first and the second GBS AI polypeptide are not the same polypeptide.
- 22. The immunogenic composition of claim 19 wherein the first GBS AI polypeptide is GBS 80 and the second GBS AI polypeptide is GBS 67.
- 23. An immunogenic composition comprising a first and a second Gram positive bacteria adhesin island (AI) polypeptide.
- 24. The immunogenic composition of claim 23 wherein the Gram positive bacteria is Streptococcus, Enterococcus, Staphylococcus, Clostridium, Corynebacterium, or Listeria.
- 25. The immunogenic composition of claim 23 wherein the first Gram positive bacteria AI polypeptide is a first Group A Streptococcus (GAS) AI polypeptide.
- 26. The immunogenic composition of claim 25 wherein the first GAS AI polypeptide is a first GAS AI-1 polypeptide.
- 27. The immunogenic composition of claim 25 wherein the first GAS AI polypeptide is a first GAS AI-2 polypeptide.
- 28. The immunogenic composition of claim 25 wherein the first GAS AI polypeptide is a first GAS AI-3 polypeptide.
- 29. The immunogenic composition of claim 25 wherein the first GAS AI polypeptide is a first GAS AI-4 polypeptide.
- 30. The immunogenic composition of any one of claims 25-29 wherein the second Gram positive bacteria AI polypeptide is a second GAS AI polypeptide.
- 31. The immunogenic composition of claim 30 wherein the second GAS AI polypeptide is a second GAS AI-1 polypeptide.
- 32. The immunogenic composition of claim 30 wherein the second GAS AI polypeptide is a second GAS AI-2 polypeptide.
- 33. The immunogenic composition of claim 30 wherein the second GAS AI polypeptide is a second GAS AI-3 polypeptide.
- 34. The immunogenic composition of claim 30 wherein the second GAS AI polypeptide is a second GAS AI-4 polypeptide.
- 35. A modified Gram positive bacterium adapted to produce increased levels of AI surface protein.

36. The modified Gram positive pacterium of claim 35 wherein the AI surface protein is in oligomeric form.

- 37. The modified Gram positive bacterium of claim 36 wherein the oligomeric form is a hyperoligomer.
- 38. The modified Gram positive bacterium of any one of claims 35-37 which is a non-pathogenic Gram positive bacterium.

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- 39. The modified Gram positive bacterium of claim 38 wherein the non-pathogenic Gram positive bacterium is *Lactococcus lactis*.
- 40. A method for manufacturing an oligomeric adhesin island (AI) surface antigen comprising:

culturing a Gram positive bacterium that expresses an oligomeric AI surface antigen and isolating the expressed oligomeric AI surface antigen.

FIGURE 1: Adhesion Island 1

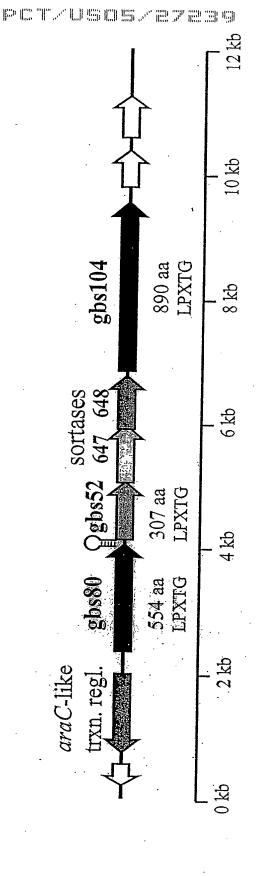


Figure 2: Conservation of AI-1 in GBS serotypes and strain isolates

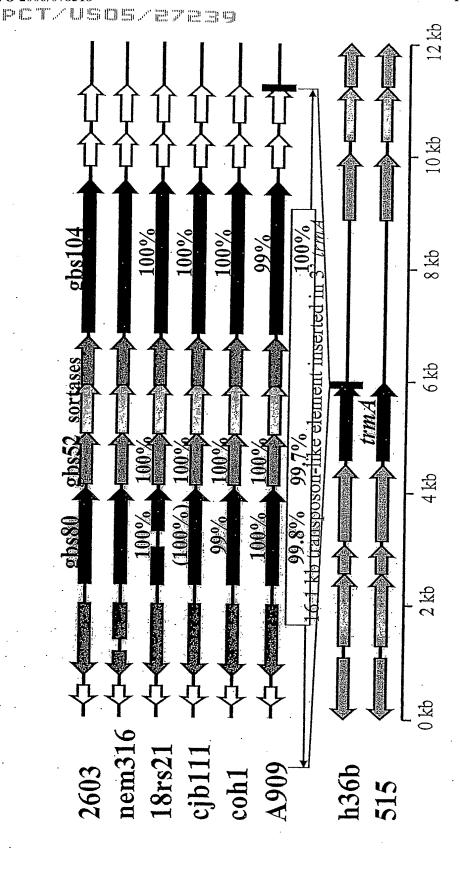
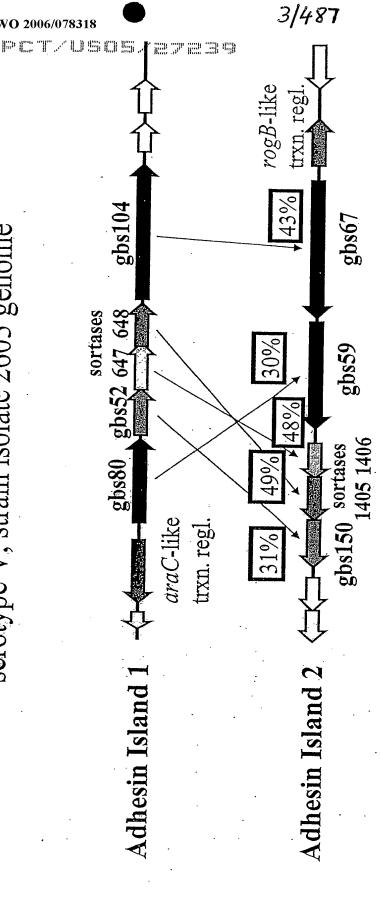
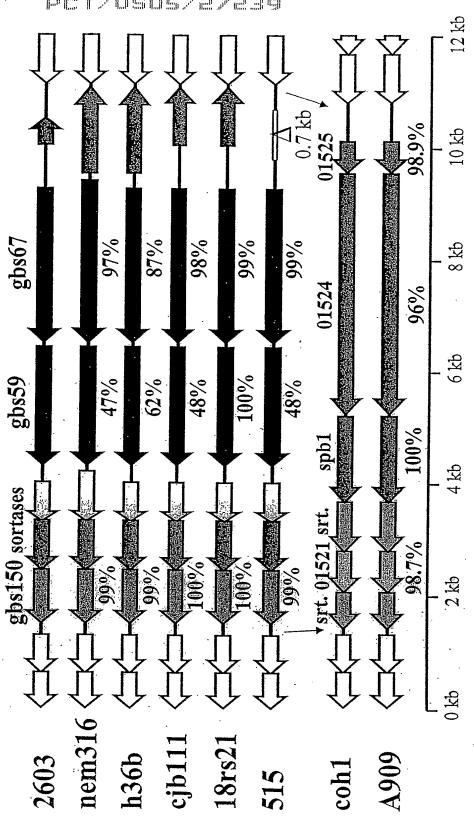


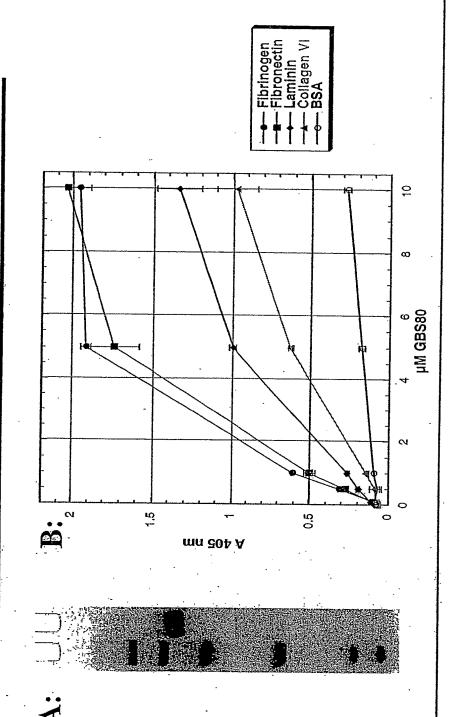
FIGURE 3: Correlation of AI-1 and AI-2 within GBS serotype V, strain isolate 2603 genome





putalsone

Figure 5: Purified gbs80 protein binds fibronectin and fibrinogen in an ELISA



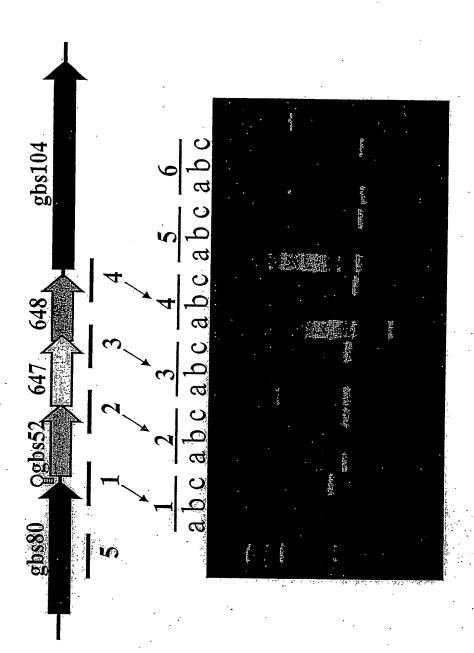
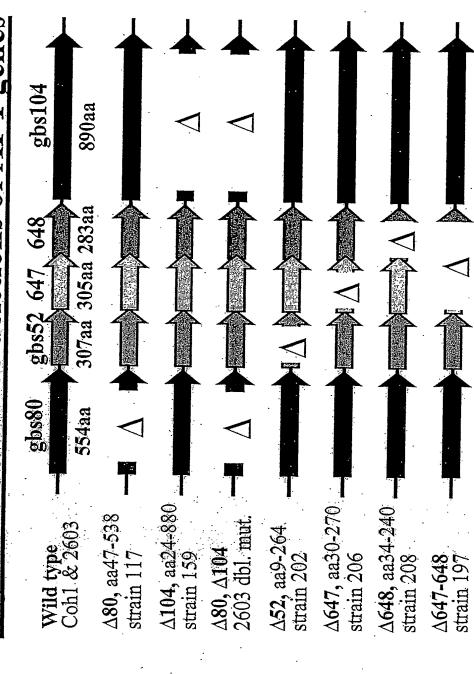
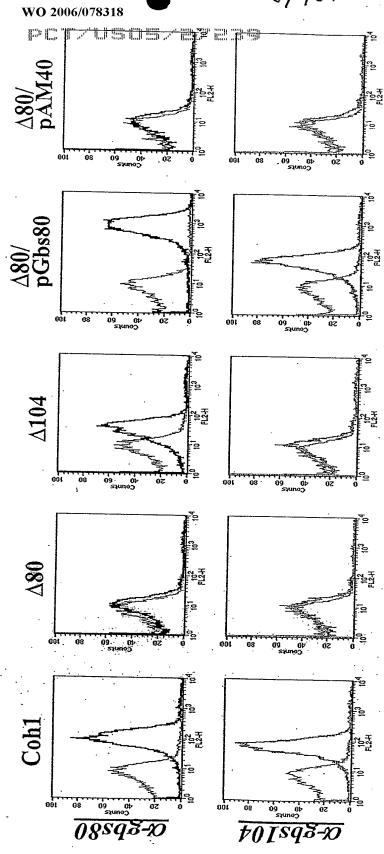
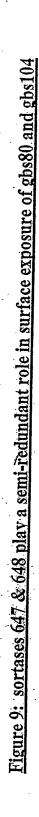
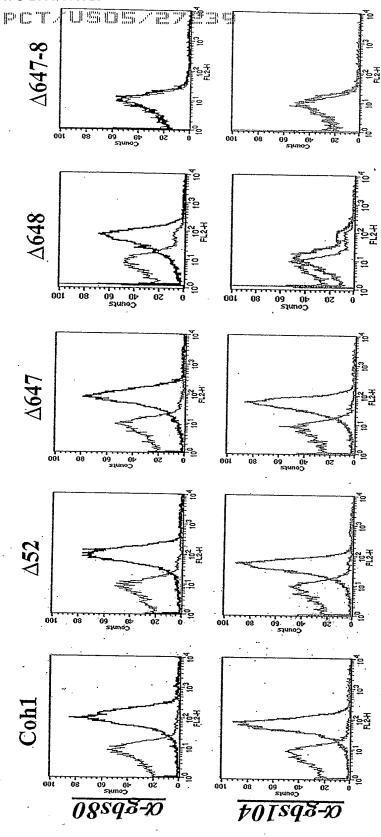


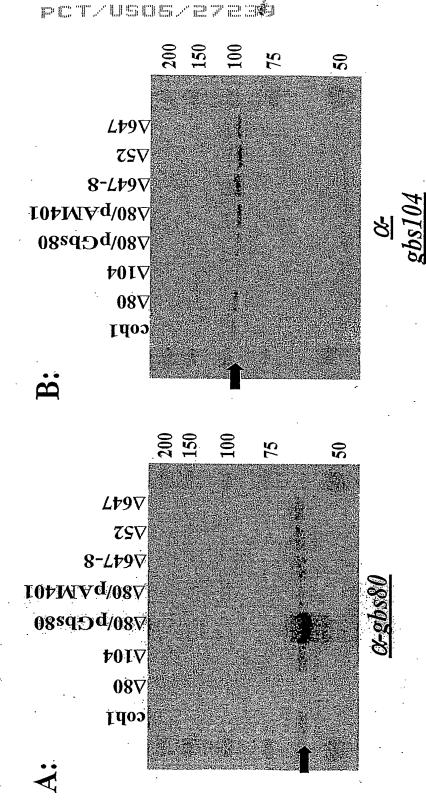
Figure 7: In frame deletions of AI-1 genes

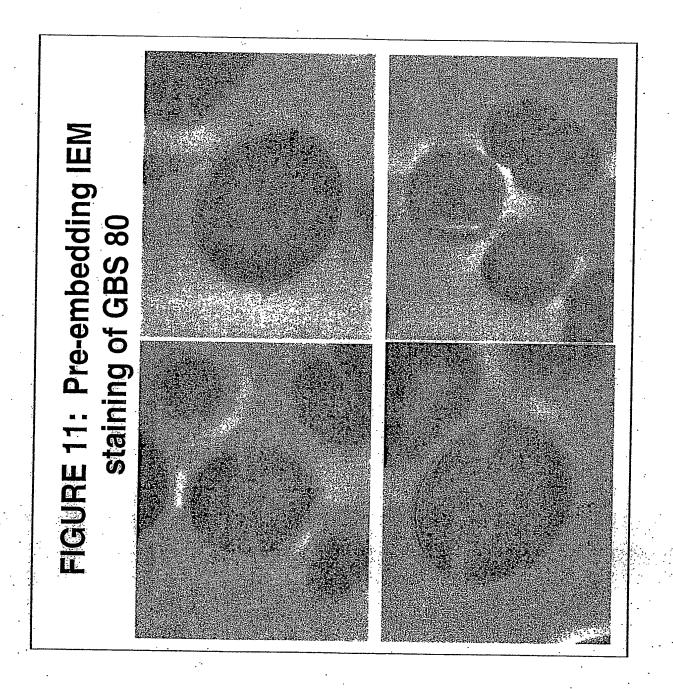












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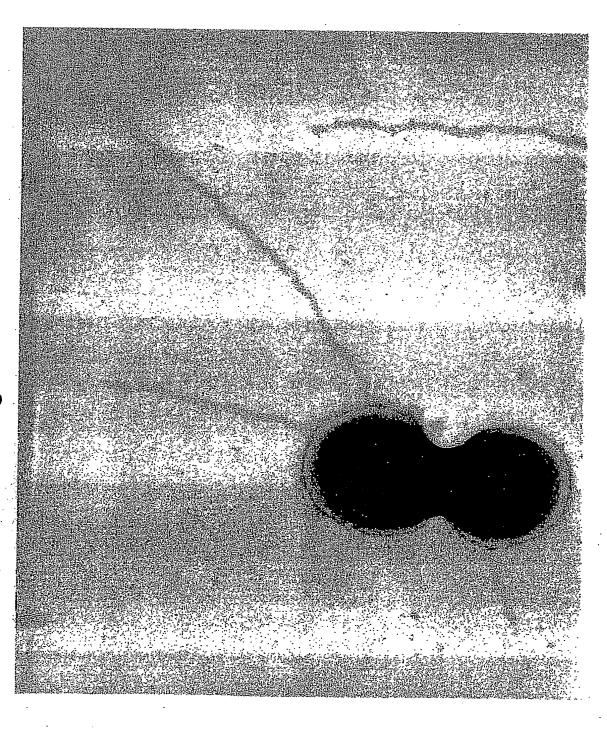
Alpha helix
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FIGURE 12: Predicted Secondary Structure for GBS 067	PREDICTION for GBS 067
	STRUCTURE
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	PHD SECC

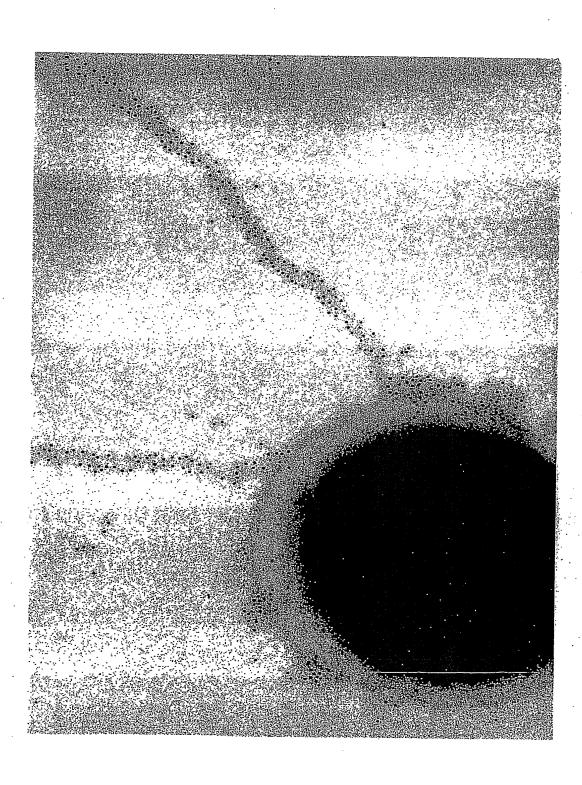
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20	FCLSQIPLNT ceeeEccccc NLIPGDYTLS	CCCCCCCCCC	CeeBBecccc OKPLDVVFVL	CCCCEREEEE KGFKEDDKYY	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	Chhhhhhhhh KPEDIKGNGE	CCCCCCC	TOIDANAIOX	EILSKIQQOF	ННИННИНН ЗСІІКСУКІЕ	CeeeceEEE	PKIKDVRBYP JCCccccCCC	KISYKDEKDG	SECEECCCC KGIIPMIGGK	CeBeeccc	901
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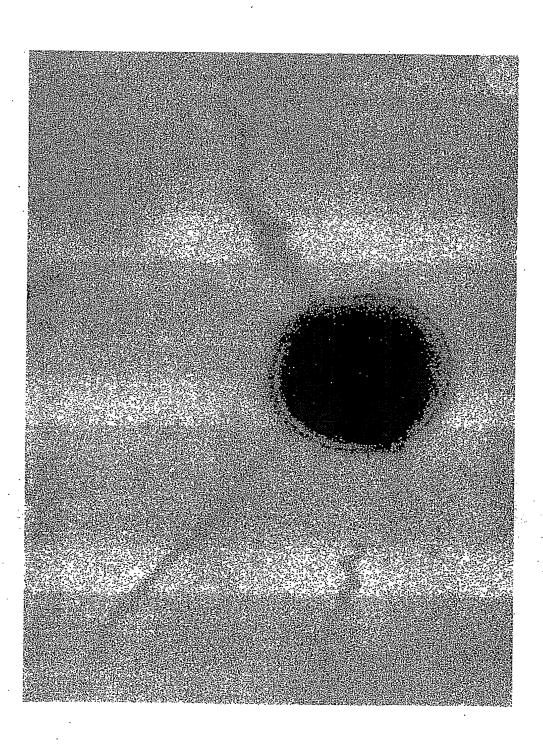


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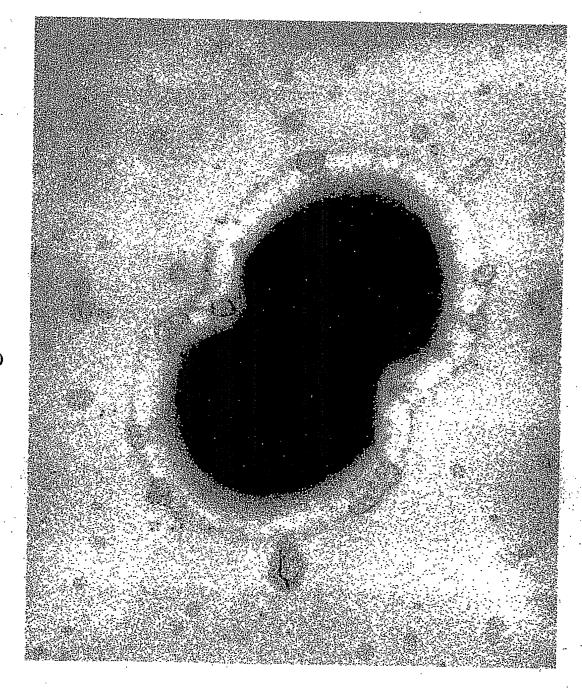
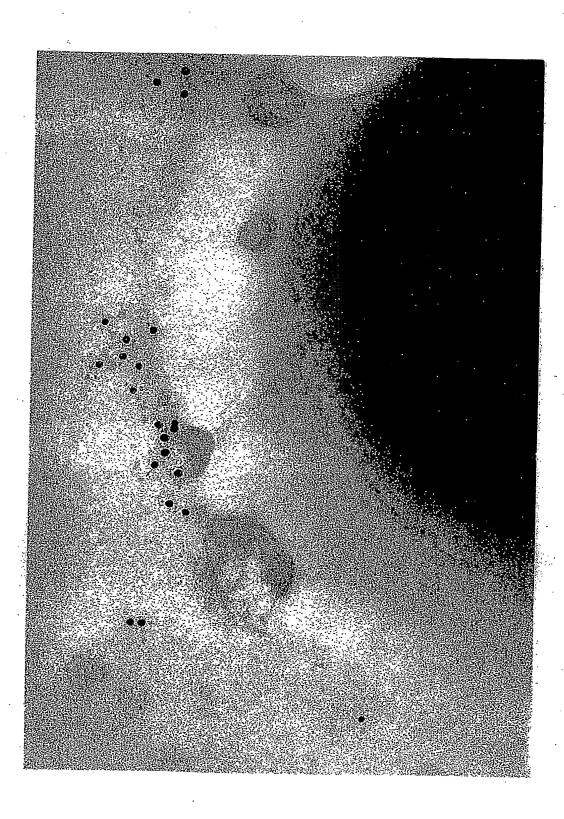
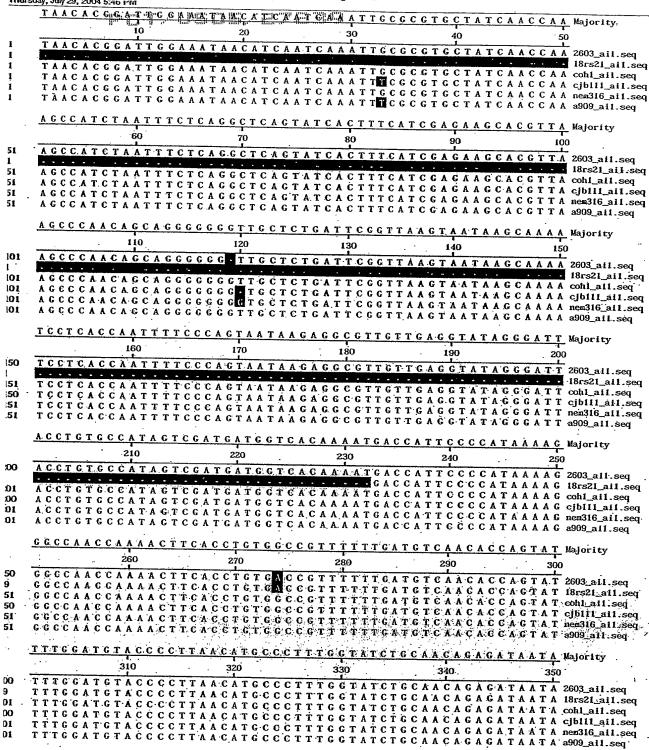


Figure 16







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Uignment Report of Al-1_alignment, using J. Hein method with Weighted residue weight table Tursday, July 29, 2004 5-46-FM. TTAGTCG"TTTCAGATGAAGGCAAAAGGATGAAATTCCGTACCTT Majority 710 720 730 740 750 TTAGTCGTTTCAGATGAAGGCAAAAGGACGATGAAATTACCCTT 2603_all.seq '00 TTAGTCGTTTCAGATGAAGGCAAAAGGATGAAATTCCGTACCTT 18rs21_aii.seq :69 T T A G T C G T T T C A G A T G A A G G C A A A A G G A C G A T G A A A T A A T T C C G T A C C T T 01cohl_ail.seq ากก TTAGTCGTTTCAGATGAAGGCAAAAGGATGAAATTCCGTACCTT cjbili_ail_seq TTAGTCGTTTCAGATGAAGGCAAAAGGACGATGAAATTCCGTACCTT nem316_ai1.seq '01 TTAGTCGTTTCAGATGAAGGCAAAAGGACGATGAAATAATTCCGTACCTT a909_a11.seq 01CATGGATTGCTATGTTACTGGCATGAGG'TCTCACGATATTTAGTAAGATA Majority 760 770 790 800 CATGGATTGCTATGTTACTGGCATGAGGTCTCACGATATTTAGTAAGATA 2603_ail,seq CATGGATTGCTATGTTACTGGCATGAGGTCTCACGATATTTAGTAAGATA 18rs21_a11.seq 19 CATGGATTGCTATGTTACTGGCATGAGGTCTCACGATATTTAGTAAGATA cohi_ai1.seq CATGGATTGCTATGTTACTGGCATGAGGTCTCACGATATTTAGTAAGATA cjbiii_ai1.seq 50 CATGGATTGCTATGTTACTGGCATGAGGTCTCACGATATTTAGTAAGATA nem316_ai1.seq CATGGATTGCTATGTTACTGGCATGAGGTCTCACGATATTTAGTAAGATA a909_ai1.seq TTCGTTTGAAGATATTCCCACGTATTTTTAAAGGTTTTAAGGAAAATGTG Majority 810 820 830 840 850 TTCGTTTGAAGATATTCCCACGTATTTTTAAAGGTTTTTAAAGAAATGTC 2603_ai1.seq TTCGTTTGAAGATATTCCCACGTATTTTTTAAAGGTTTTAAAGAAATGTG 18rs21_a11.seq TTCGTTTGAAGATATTCCCACGTATTTTTAAAGGTTTTAAAGAAATGTG cohl_ail.seq TTCGTTTGAAGATATTCCCACGTATTTTTTAAAGGTTTTTAAAGAAATGTG cjbiii_aii.seq TTCGTTTGAAGATATTCCCACGTATTTTTAAAGGTTTTTAAAGAAATGTG nem316_ail.seq TTCGTTTGAAGATATTCCCACGTATTTTTAAAGGTTTTAAGAAATGTG a909_ail.seq TGGTGTCGTAAAAATGTAATTTCGCTACTTCCCCAATCGGTACCCCT Majority 860 880 890 TGGTGTCGTAAAAATGTAATTTCGCTACTTCCCCAATCGGTACCCCT 2603_ail.seq TGGTGTCGTAAAAATGTAATAATTTCGCTACTTCCCCAATCGGTACCCCT 18rs21_ai1.seq 19 TGGTGTCGTAAAAATGTAATAATTTCGCTACTTCCCCAATCGGTACCCCT cohl_ail.seq TGGTGTCGTAAAAATGTAATAATTTCGCTACTTCCCCAATCGGTACCCCT cjb111_a11.seq TGGTGTCGTAAAAATGTAAT/AATTTCGCTACTTCCCCAATCGGTACCCCT nem316_ai1.seq T G G T G T C G T A A A A A T G T A A T A A T T T C G C T A C T T C C C C A A T C G G T A C C C C T a909_ai1.seq CTTTGCAGTAGTAATTGTCCCTTAATTTTTGCCTTTAGAATATAACT Majority 910 920 930 940 950 CTTTGCAGTAGTAATTGTCCCTTCATTTTTGCCTTTAGAATATAACT 2603_ail.seq CTTTGCAGTAGTAATTGTCCCTTCATTTTTGCCTTTAGAATATAACT 18rs21_ai1.seq **39** CTTTGCAGTAGTAATTGTCCCTTCATTTTTGCCTTTAGAATATAACT cohl_ail.seq CTTTGCAGTAGTAATTGTCCCTTCATTTTTGCCTTTAGAATATAACT cjblil_ai1.seq 10 CTTTGCAGTAGTAATTGTCCCTTAATTTTTGCCTTTAGAATATAACT a909_ail.seq TTCCAAGGAAATCTCAGACTATTTTTAAAAACTGAGCGTAAGTCGGAAT Majority 960 970 980 990 1000 TTGCAAGGAAATGTCAGAGTATTTTTAAAAACTGAGCGTAAGTCGGAAT 2603_all.seq TTCCAACCAAATGTCACAGTATTTTTAAAAACTGACCGTAAGTGGGAAT 18rs21 all seq TT. G C A A G G A A A T G T C A G A G T A T T T T T T A A A A A C T G A G C G T A A G T G G G A A T cohl_all seq TTGCAAGGAAATGTCAGAGTATTTTTTAAAAAGCGAAGCGTAAGTGGCAAT cjbiii ail seq TTGCAAGGAAATGTCAGAGTATTTTTTAAAAAGCGAAGCGAAGTGGAAT nem316 ail seq TTGCAAGGAAATGTCAGAGTATTTTTTAAAAAACCGAAGCGAAGTGGAAT a909 ail seq CTGAGATATACGTAGTTGGCAATATCAGATACTTTGAGTTTGGAGTAG Majority 1010 1020 1030 1040 CTGAGATATATAGGTAGTTGGCAATATCAGATACTTTGAGTTTGGAGTAG 2603_aii.seq 100 C.T.G. A.G. A.T. A.T. A.G. G.T. A.G.T.T.G.G.C. A.A.T. A.T.C. A.G.A.T. A.C.T.T.G.G.A.G.T.T.G.G.A.G.T.A.G. 18rs21_ai1.seq CTGAGATATATAGGTAGTTGGCAATATCAGATACTTTGAGTTTGGAGTAG cohlail.seq ÒΙ 100 TTGAGATATATAGGTAGTTGGCAATATCAGATACTTTGAGTTTGGAGTAG cjbii1_ai1.seq

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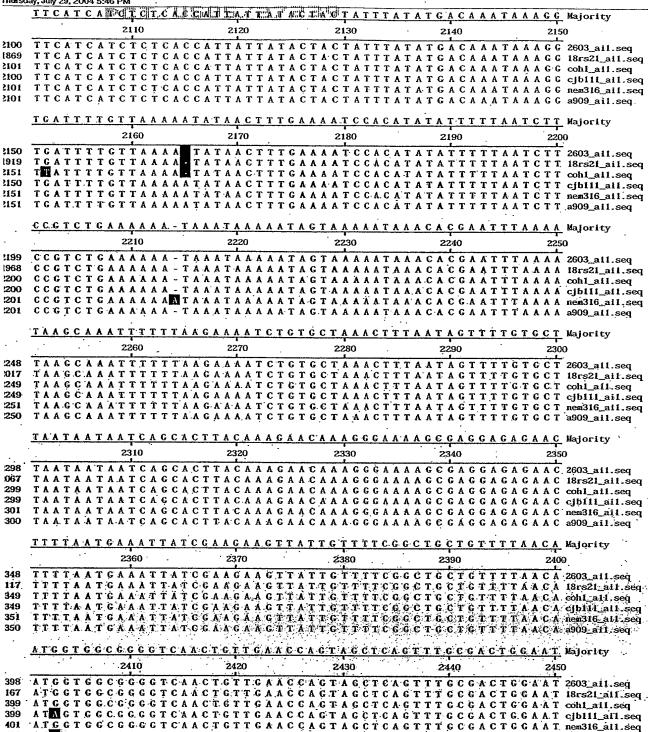
Alignment Report of Al-1_alignment, using J. Hein method with Weighted residue weight table. Thursday, July 29, 2004 5;46 P.M. ... AT CONCATTACTATTACATTTCCTCCTC Majority AGGTGGTTCTCCAC 1060 1070 1080 1090 1100 AGGTGGTTGTCCACATAATGGAGAATACTATTGTACATTTGCTGCTGCTTGTC 2603_ail.seq. 1050 A G G T G G T T G T C C A C A T A A T G G A C A A T A C T A T T G T A C A T T T G C T G C T T G T C 18rs21_ai1.seq A G G T G G T T G T C C A C A T A A T G G A G A A T A C T A T T G T A C A T T T G C T G C T T G T C cohl_ail.seq 1051 A G G T G G T T G T C C A C A T A A T G G A G A A T A C T A T T G T A C A T T T G C T G C T T G T C cjbili_aii.seq A G G T G G T T G T C C A C A T A A T G G A G A A T A C T A T T G T A C A T T T G C T G C T T G T C nem316_ai1.seq A G G T G G T C C C C A C A T A A T G G A G A A T A C T A T T G T A C A T T T G C T G C T T G T C a 909_ail.seq A G A G A T G C T C T T A T T G G T T A A G G A T T C T G A A A A T C A A T A A G A G C T G C A C Majority 1110 1130 1140 1150 A G.A G A T G C T C T T A T T G G T T A A G G A T T C T G A A A A A T C A A T A A G A G C T G C A C 2603_ail.seq 1100 A GAGATGCTCTTATTGGTTAAGGATTCTGAAAAATCAATAAGAGCTGCAC 18rs21_ai1.seq A G A G A T G C T C T T A T T G G T T A A G G A T T C T G A A A A A T C A A T A A G A G C T G C A C coh1_ai1.seq 1101 A G A G A T G C T C T T A T T G G T T A A G G A T T C T G A A A A T C A A T A A G A G C T G C A C cjbiii_ail.seq 1100 A G A G A T G C T C T T A T T G G T T A A G G A T T C T G A A A A A T C A A T A A G A G C T G C A C nem316_ai1.seq 1101 A G A G A T C C T C T T A T T C G T T A A G G A T T C T G A A A A A T C A A T A A G A G C T G C A C a909_a11.seq A G C G A A T T C T T G A A A C A T C A A T A A G A T C A G G A G C C T C T T C G T T T A A A G C C Majority 1170 1160 1180 1190 1200 A G C G A A T T C T T G A A A C A T C A A T A A G A T C A G G A G C C T C T T C G T T T A A A G C C 2603_ai1.seq 1150 319 A G C G A A T T C T T G A A A C A T C A A T A A G A T C A G G A G C C T C T T C G T T T A A A G C C 18rs21_ail.seq A G C G A A T T C T T G A A A C A T C A A T A A G A T C A G G A G C C T C T T C G T T T A A A G C C cohlail.seq 1151 A G C C A A T T C T T G A A A C A T C A A T A A G A T C A G G A G C C T C T T C G T T T A A A G C C cjbiii_aii.seq 1150 A G C C A A T T C T T G A A A C A T C A A T A A G A T C A G G A G C C T A T T C G T T T A A A G C C nem316 ail.seq 1151 A G C G A A T T C T T G A A A C A T C A A T A A G A T C A G G A G C C T C T T C G T T T A A A G C C a909_ail.seq 1151 A T A T A G T G C T T T A C C A G C G C A T A A C T T T T A G C C A C A T C A G T A T T T T C C T C Majority 1220 1210 1230 1240 1250 ATATAGTGCTTTACCAGCGCATAACTTTTAGCCACATCAGTATTTTCCTC 2603_ail.seq 1200 ATATAGTGCTTTACCAGCGCATAACTTTTAGCCAACATCAGTATTTTCCTC 18rs21_ai1.seq 169 ATATAGT GCTTTACCAGCGCATAACTTTTAGCCACATCAGTATTTTCCTC cohlail.seq 201 1200 ATATAGTGCTTTACCAGCGCATAACTTTTAGCCACATCAGTATTTTTCTC cjbli1_ail.seq ATATAGTGCTTTACCAGCGCATAACTTTTAGCCAACATCAGTATTTTCCTC nem316_ai1.seq 201 1201 ATATAGTGCTTTACCAGCGCATAACTTTTAGCCAATCAGTATTTTCCTC a909_ai1.seq GAAACTTAATTCTAGTAATTTTGTTAAGTAAACAACAGTTAAGTTCTTTT Majority 1260 1280 1290 1300 GAAACTTAATTCTAGTAATTTTGTTAAGTAAACAACAGTTAAGTTCTTTT 2603_ail.seq GAAACTTAATTCTAGTAATTTTGTTAAGTAAACAACAGTTAAGTTCTTTT 18rs21_a11.seq 019 GAAACTTAATTCTAGTAATTTTGTTAAGTAAACAACAGTTAAGTTCTTTT cohlail.seq GAAACTTAATTCTAGTAATTTTGTTAAGTAAACAACAGTTAAGTTCTTTT cjbiil_ail.seq GAAACTTAATTCTAGTAATTTTGTTAAGTAAACAACAGTTAAGTTCTTTT nem316_ail.seq GAAACTTAATTCTAGTAATTTTGTTAAGTAAACAACAGTTAAGTTCTTTT a909_ail.seq C A G C T C T T A G G G C A G G G A T T G A A G A T G A GGTAACACTGGATGATGGGAGG Majority 1310 1320 1330 1340 1350 CAGCTCTTAGGGCAGGGATTGAAGATGAGGTAACACTGGATGATGGGAGG 2603 ail seq CAGCTCTTAGGGGAGGATTGAAGATGAGGTAACACTGGATGATGGGAGG 18rs21 ail seq CAGCTCTTAGGGGAGGATTGAAGATGAGGTAACACTGGATGATGGGAGG cohlail seq 300 069 301 CAGCTCTTAGGGCAGGGATTGAAGATGAGGTAACACTGGATGGGAAGGGGBIH att seq 300 301 CACCTCTTAGGGGCATTGAAGATGAGGTAACACTGGATGATGGGAGG as09 all seq 301 C G A T T A A T T T C T T G C T T T A A C A G T T G A G T G T T A C C C A G C T T A A C G A G A T C Majority 1360 1370 . 1380. . 1390 1400 C G A T T A A T T T C T T G C T T T A A C A G T T G A G T G T T A C C C A G C T T A A C G A G A T C 2603_ail.seq 350 CGATTAATTTCTTGCTTTAACACTTGAGTGTTACCCAGCTTAACGAGATC 18rs21_ai1.seq 119 C G A T T A A T T T C T T G C T T T A A C A G T T G A G T G T T A C C C A G C T T A A C G A G A T C cohi_ail.seq C G A T T A A T T T C T T C C T T T A A C A G T T G A G T G T T A C C C A G C T T A A C G A G A T C. cjbili_aii.seq C.G.A.T.T.A.A.T.T.C.T.T.G.C.T.T.T.A.A.C.A.G.T.T.G.A.G.T.G.T.T.A.C.C.C.A.G.C.T.T.A.A.C.G.A.G.A.T.C. nem316_ail.seq

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ignment Report of Al-1_aignment, using J. Hein method with Weighted residue weight table. hursday, July 29, 2004 5:46 PM AATAATGT GAATTT GALGATTT MAGACT GTGGT AACTGAAAAGAGTTTT Majority 1420 1430 1440 AATAATGTGATTGAGATGGTTTAAAAACAGTGGGTAACTGAAAAGAGTTTT 2603_ail.seq 400 AATAATGTGATTGAGATGGTTTAAAACAGTGGGTAACTGAAAAGAGTTTT 18rs21_ai1.seq 169 AATAATGTGATTGAGATGGTTTAAAACAGTGGGTAACTGAAAAGAGTTTT cohl_ail.seq 401 AATAATGTGATTGAGATGGTTTAAAACACTGGGTAACTGAAAAGAGTTTT cjb111_ai1.seq 400 AATAATGTGATTGAGATGGTTTAAAACAGTGGGTAACTGAAAAGAGTTTT nem316_ail.seq 401 A A T A A T C T C A T T G A C A T G C T T T A A A A C A C T C C C T A A C T G A A A A C A C T T T T a909_aii.seq 401 TCTTAGTATGTTTTAGGTGAAGAACAATATCAGGATCCGCAACAATCTGT Majority 1460 1470 1480 1490 TCTTAGTATGTTTAGGTGAAGAACAATATCAGGATCCGCAACAATCTGT 2603_ai1.seq 450 TCTTAGTATGTTTAGGTGAAGAACAATATCAGGATCCGCAACAATCTGT 18rs21_ail.seq 219 TCTTAGTATGTTTTAGGTGAAGAACAATATCAGGATCCGCAACAATCTGT coh1_ai1.seq 451 TCTTAGTATGTTTAGGTGAAGAACAATATCAGGATCCGCAACAATCTGT cjb111_ai1.seq 450 TCTTAGTATGTTTAGGTGAAGAACAATATCAGGATCCGCAACAATCTGT nex316_ail.seq 451 TCTTAGTATGTTTAGGTGAAGAACAATATCAGGATCCGCAACAATCTGT a909_ai1.seq 451 TCTGACTCTTCTAATAAATGATTGATGGCTTGTTGGCAACTAGCCTCAAA Wajority 1510 1520 1530 1540 1550 TCTGACTCTTCTAATAAATGATTGATGACTTGTTGGCAACTAGCCTCAAA 2603_ai1.seq 500 TCTGACTCTTCTAATAAATGATTGATGACTTGTTGGCAACTAGCCTCAAA 18rs21_ail.seq 269 TCTGACTCTTAATAAATGATTGATGACTTGTTGGCAACTAGCCTCAAA cohlall.seq 501 TCTGACTCTTCTAATAAATGATTGATGGCTTGTTGGCAACTAGCCTCAAA cjb111_a11.seq 500 TCTGACTCTACTAATAAATGATTGATTGGCTTGGCAACTAGCCTCAAA niem316_ail.seq 501 TCTGACTCTTAATAAATGATTGATGGCTTGTTGGCAACTAGCCTCAAA a909_a11.seq CTGTGTTTGGAAAAGGCATCGATAGACACAAGACTACGTATACTGG Majority 1560 1570 1580 1590 1600 550 CTGTGTTTGGAAAAGGCCATCGATAGACACAAGAAGACTACGTATACTGG 18rs21_ail.seq 319 CTGTGTTTGGAAAAAGGCATCGATAGACACAAGAAGACTACGTATACTGG cohl_ai1.seq 551 550 CTGTGTTTGGAAAAGGCATCGATAGACACAAGAAGACTACGTATACTGG cjbiii_ai1.seq CTGTGTTTGGAAAAAGGCATCGATAGACAAAAAGACTACGTATACTGG nem316_ai1.seq 551 CTGTGTTTGGAAAAAGGCATCGATAGACACAAGAAGACTACGTATACTGG a909_ai1.seq TAGTAGGAAAACAAGGGACAAGCTTTATAGGATAAGATTTCTTTTA Majority 1610 1620 1630 1640 TAGTAGGAAAACAAGGGACAAGCTTTATAGGATAAGATTTCTTTTTA 2603_aii.seq TAGTAGGAAAACAAGGGACAAGCTTTATATAGGATAAGATTTCTTTTTTA 18rs21_ail.seq TAGTAGGAAAACAAGGGACAAGCTTTATATAGGATAAGATTTCTTTTTA cohl_ail.seq 106 TAGTAGGAAAACAAGGGACAAGCTTTATATAGGATAAGATTTCTTTTTA cjbli1_ail.seq 900 TAGTAGGAAAACAAGGGACAAGCTTTATATAGGATAAGATTTCTTTTTA nem316_ail.seq. Ю1 TAGTAGGAAAACAAGGGACAAGCTTTATATAGGATAAGATTTCTTTTTA a909_ail.seq. CTACGATGAGAAATTGTTCTAGAAAGCGACTGGATAACTGTTCTTGCCT Majority 1660 1670 1680 1690 1700 150 TTACGATGAGAAAATTGTTCTAGAAAGCGACTGGATAACTGTTCTTGCCT 2603_ail.seq 119 CTACGATGAGAAAATTGTTCTAGAAAGCGACTGGATAACTGTTCTTGCCT 18rs21_ail.seq CTACGATGAGAAAATTGTTCTAGAAAGCGACTGGATAACTGTTCTTGCCT cohlail seq CTACGATGAGAAAATTGTTCTAGAAACCGACTGGATAACTGTTCTTGCCTGGLAH seq CTACGATGAGAAATTGTTCTAGAAAGCGACTGGATAACTGTTCTTGCCTTAGAAAGCGATACCTGTTCTTTGCTTAGAAAGCGATACCTGTTCTTTGCTTAGAAAGCGACACACTGTTCTTTGCTTTGCTTAGAAAGCGACTGTAGAAACTGTTTCTTTGCTT ATTGATATCAGGGCTATAGGGATAAAATGGTCCAATAGCAATAAGATATT Majority 1710 1720 1730 1740 1750 ATT GATATCA GGGCTTATA GGGATAAAAT GGTCCAATAGCAATAA GATATT :2603_aii.seq ATTGATATCAGGGGTATAGGGATAAATGGTCCAATAGCAATAAGATATT 18rs21_a11.seq 69 10 ATT GATAT CAG G G CTATA G G G ATAAAAT G G T C C AATAG CAATAA G ATAT Cohi_ail.seq ATTGATATCAGGGCTATAGGGATAAAATGGTCCAATAGCAATAAGATATT cjb111_ai1.seq '00 ATTGATATCAGGGGTATAGGGATAAATGGTCCAATAGCAATAAGATATT nem316_all.seq OI

ATTGATATCAGGGCTATAGGGATAAAATGGTCCAATAGCATAAGATT a909_a11.seq

hursday, July 29, 2004 5:46 PM 1760 1770 1780 1790 1800 GACAGACAGGAAAATTAAGAATGATTCTTCAAAAAGACCCTCATAAACA 2603_ai1.seq .750 GACAGACAGGAAAATTAAGAATGATTCTTCAAAAAGACCCTGATAAACA 18rs21_ai1.seq 519 GACAGACAGGAAAATTAAGAATGATTCTTCAAAAAGACCCTCATAAACA cohl_ail.seq 751 GACAGACAGGAAAATTAAGAATGATTCTTCAAAAAGACCCTCATAAACA cjbii1_ai1.seq 750 GACAGACAGGAAAAATTAAGAATGATTCTTCAAAAAGACCCCTCATAAACA nex316_ai1.seq 751 GACAGACAGGAAAATTAAGAATCTTCAAAAAGATCCTCATAAACA a909_ai1.seq 751 GTGATATCTTGGTTATAAGGGATAGCTAAATGTTTTAAAAAACTGATAGTA Majority 1810 1820 1830 1840 1850 CTGATATCTTGGTTATAAGGGATAGCTAAATGTTTTAAAAACTGATAGTA 2603_ai1.seq 800 GTGATATCTTGGTTATAAGGGATAGCTAAATGTTTTAAAAACTGATAGTA 18rs21_ai1.seq 569 GTGATATCTTGGTTATAAGGGATAGCTAAATGTTTTAAAAACTGATAGTA cohl_ail.seq 801 GTGATATCTTGGTTATAAGGGATAGCTAAATGTTTTAAAAACTGATAGTA cjbiil_ail.seq ROO GTGATATCTTGGTTATAAGGGATAGCTAAATGTTTTAAAAACTGATAGTA nem316_ail.seq 801 GTGATATCTTGGTTATAAGGGATAGCTAAATGTTTTAAAAACTGATAGTA a909_ai1.seq ACCCAACAGATAGTCTTCGTTACCATATAACTGAACGAGTTCCTTGTCTC Majority 1860 1870 1880 1890 A G G C A A C A G A T A G T C T T C G T T A C C A T A T A A C T G A A C G A G T T C C T T G T C T C 2603_ai1.seq 850 AGGCAACAGATAGTCTTCGTTACCATATAACTGAACGAGTTCCTTGTCTC 18rs2f_ai1.seq 619 AGGCAACAGATAGTCTTCGTTACMATAACTGAACGAGTTCCTTGTCTC cohl ail. seq 851 A G G C A A C A G A T A G T C T T C G T T A C C A T A T A A C T G A A C G A G T T C C T T G T C T C ejbli1_ail.seq 850 A G G C A A C A G A T A G T C T T C G T T A C C A T A T A A C T G A A C G A G T T C C T T G T C T C nem316_ai1.seq A G G C A A C A G A T A G T C T T C G T T A C C A T A T A A C T G A A C G A G T T C C T T G T C T C a909_a11.seq GTGACATGACTGAAATAGGTAGTTGAGATATCGTATGCAATGTTTGAACA Majority 1920 1940 1950 GTGACATGACTGAAATAGGTAGTTGAGATATGGTATGCAATGTTTGAACA 2603_ai1.seq GTGACATGACTGAAATAGGTAGTTGAGATATGGTATGCAATGTTTGAACA 18rs21_ai1.seq GTGACATGACTGAAATAGGTAGTTGAGATATGGTATGCAATGTTTGAACA cohl_all.seq 900 GTGACATGACTGAAATAGGTAGTTGAGATATGGTATGCAATGTTTGAACA cjb111_ai1.seq GTGAGATGACTGAAATAGGTAGTTGAGATATGGTATGCAATGTTTGAACA nem316_ai1.seq GTGACATGACTGAAATAGGTAGTTGAGATATGGTATGCAATGTTTGAACA a909_a11.seq T G T T T A A A A T C G A A T G T A A C C A T T T G A T A G A C C G C C T T C A T T A T C A T T T C Majority 1960 1970 1980 1990 2000 TGTTTAAAATCGAATGTAACCATTTGATAGACCGCCTTCATTATCATTTC 2603_ai1.seq 950 TGTTTAAAATCGAATGTAACCATTTGATAGACCGCCTTCATTATCATTTC 18rs21_ai1.seq 719 T G T T T A A A A T G G A A T G T A A C C A T T T G A T A G A C C G C C T T C A T T A T C A T T T C 951 T G T T T A A A T C G A A T G T A A C C A T T T G A T A G A C C G C C T T C A T T A T C A T T T C cjbii1_ai1.seq 950 TGTTTAAAATCGAATGTAACCATTTGATAGACCGCCTTCATTATCATTTC nem316_all.seq 951 T G T T T A A A A T C G A A T G T A A C C A T T T G A T A G A C C G C C T T C A T T A T C A T T T C a909_ail.seq TAGAATTTTCTTTAGGTTTGTAAAGACTACAAAATAAAATGATGAAAAC Majority 2010 2020. 2030 2040 2050 TAGAATTTTTCTTTAGGTTTGTAAAGACTACAAAATAAAATGATGAAAC 18rs21 all seq TACAATTTTCTTTAGGTTAGAAGACTACAAAATAAAATGATGAAAC cont. att. seq TAGAATTTTTCTTTAGGTTAGGTTAGAAGAGTACAAATAAAATGATGATGAAAAAC ejberrari seq TAGAATTTTTCTTAGGTTTGTAAAGACTACAAATAAAATGATCAAAAG AACTATCTTGTGGATACACTAAAAGCCCTAATTAGCAAACTCTCTC Majority 2060 2070 2090 2080 2100 AACTATCTTGTGGATACACTAAAAGACACGCTAATTAGCAAACTCTCTC 2603_a11.seq)50 AACTATCTTGTGGATACACTAAAAGACACGCTAATTAGCAAACTCTCTC 18rs21_a11.seq 319 AACTATCTTGTGGATACACTAAAAAGACACGCTAATTAGCAAACTCT,CTC cohlaii.seq 151 AACTATCTTGTGGATACACTAAAAAGACACGCTAATTAGCAAACTCTCTC cjbill_ai1.seq 150 A A C T A T C T T C T G G A T A C A C T A A A A A G A C A C C C T A A T T A G C A A C T C T C T C nem316 ail. seq 351 A A C T A T C T T G T G G A T A C A C T A A A A A G A C A C G C T A A T T A G C A A A C T C T C T C a909_a11.seq 351



ATA GT G G C G G G T C A A C T G T T G A A C C A G T A G C T C A G T T T G C G A C T G G A A T a909_ail.seq.

Alignment Report of Al-1_WO 2006/078318 Thursday, July 29, 2004 5:46 PM A C'A COT CE OF A A CAA CAA CAA CCC CCAG CGAAAA CAA Majority GAGTATTET 2460 2480 2490 GAGTATTGTAAGAGCTGCAGAAGTGTCACAAGAACGCCCAGCGAAAACAA 2603_ai1.seq 2448 GAGTATTGTAAGAGCTGCAGAAGTGTCACAAGAACGCCCAGCGAAAACAA 18rs21_ai1.seq 2217 GAGTATTGTAAGAGCTGCAGAAGTGTCACAAGAACGCCCAGCGAAAACAA cohi_ail.seq 2449 GAGTATTGTAAGAGCTGCAGAAGTGTCACAAGAACGCCCAGCGAAAACAA cjb111_ai1.seq 2449 GACTATTGTAAGAGCTGCAGAAGTGTCACAAGAACCCCCAGCGAAAACAA nem316_aii.seq 2451 2450 GAGTATTGTAAGAGCTGCAGAAGTGTCACAAGAACGCCCAGCGAAAACAA a909_ail.seq CAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTACT Majority 2510 2520 2530 2540 2550 CAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTACT 2603_ai1.seq 2498 CAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTACT 18rs21_a11_seq 2267 CAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTACT cohl_ail.seq CAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTACT cjbiii_aii.seq 1499 CAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTACT nem316_a11.seq CAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTACT a909_ail.seq TCTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTATGC Majority 2560 2580 2590 TCTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTATGC 2603_all.seq :548 TCTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTATGC 18rs21_a11.seq T.CTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTATGC cohl_ail.seq TCTAATGGTGGTATCGAGAATAAAGACGCCGAAGTAATATCTAACTATGC cjbiii_aii.seq T.C.T.A.A.T.G.G.T.G.G.A.G.A.A.T.A.A.G.A.C.G.G.C.G.A.A.G.T.A.T.C.T.A.A.C.T.A.T.G.C. nem316_a11.seq T C T A A T G G T G G T A T C G A G A A T A A A G A C G G C G A A G T A A T A T C T A A C T A T G C a909_ail.seq T A A A C T T G G T G A C A A T G T A A A A G G T T T G C A A G G T G T A C A G T T T A A A C G T T Majority 2620. 2630 2640 2650 TAAACTTGGTGACAATGTAAAAGGTTTGCAAGGTGTACAGTTTAAAACGTT 2603_ail.seq TAAACTTGGTGACAATGTAAAAGGTTTGCAAGGTGTACAGTTTAAACGTT 18rs21_ai1.seq TAAACTTGGTGACAATGTAAAAGGTTTGCAAGGTGTACAGTTTAAACGTT cohi_ail.seq TAAACTTGGTGACAATGTAAAAGGTTTGCAAGGTGTACAGTTTAAACGTT cjbiii_aii.seq TAAACTTGGTGACAATGTAAAAGGTTTGCAAGGTGTACAGTTTAAACGTT nem316_ai1.seq TAAACTTGGTGACAATGTAAAAGGTTTGCAAGGTGTACAGTTTAAACGTT a909_aii.seq AAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAATTGACAACA Majority 2660 2680 2690 ATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAATTGACAACA 2603_a11.seq 648 417 ATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAATTGACAACA 18rs21_ai1.seq ATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAACA cohl_ail.seq 649 ATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAATTGACAACA cjbii1_ai1.seq 549 ATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAATTGACAACA nem316_ail.seq ATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAACA a909_aii.seq GTTGAAGCAGCACATCCAAAGTTGGAACGATTCTTGAAGGTGTCAG Majority 2710 2720 2730 2740 2750 GTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGCTCTCAC 2603_ai1.seq GTTGAAGCAGCAGATGCAAAAGTTCGAACCATTCTTGAAGGTGTCAG 18rs21_ai1.seq GTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTCAG nem316 att seq GTTGAAGCAGGATGCAAAAGTTCGAACGATTCTTGAAGAAGGTCTCAG agog ail seq TCTACCTCAAAAACTAATGCTCAAGGTTTGGTCGTCGATGCTCTGGATT Majority 2760 2770 2780 2790 2800 TCTACCTCAAAAACTAATGCTCAAGGTTTGGTCGTCGATGCTCTCGATT 2603_a11.seq **'48** TCTACCTCAAAAACTAATGCTCAAGGTTTGGTCGTCGATGCTCTGGATT 18rs21_ai1.seq 117 49 TCTACCTCAAAAAACTAATCCTCAAGGTTTGGTCGTCGATGCTCTGGATT cont_ai1.seq ÚΩ TCTACCTCAAAAAACTAATGCTCAAGGTTTGGTCGTCGATGCTCTGGATT cjbii1_aii.seq

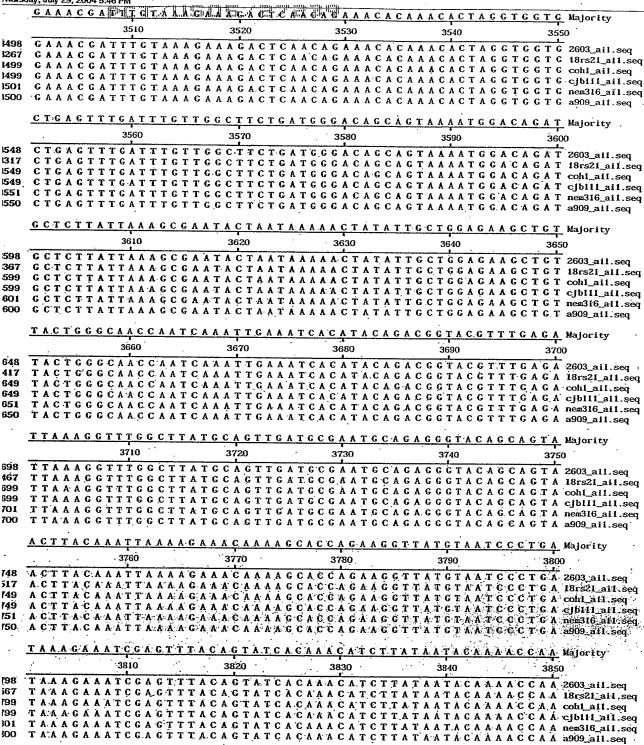
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TCTACCTCAAAAAACTAATGCTCAAGGTTTGGTCGATGCTCTGGATT a909_a11.seq

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	26/4	
Alignm Thursd	ment Report of Al-1 \underline{WO} $\underline{2006/078318}$ method with Weighted residue weight table day, July 29, 2004 5:46 PM	PCT/US2005.
	CAAAAAG BAAT GTGAGATACTIT GTATA TA GAAG	GATTTAAAGAATTCACCT Majority
•	2810 2820 2830	2840 2850
798 .	. CAAAAAGTAATGTGAGATACTTGTATGTAGAAG	GATTTAAAGAATTCACCT 2603 all seg
567 799		2 A T T T A A A C A A T T C A C C T 1021 -11
799	CAAAAAGTAATGTGAGATACTTGTATGTAGAAG	GATTTAAAGAATTCACCT cohl_all.seq
301	- VAAAAGTAATGTGAGATACTTCTATCTACAAC	ATTTAAACAATTCACCT ==1010 =11
300	CAAAAGTAATGTGAGATACTTGTATGTA'GAAG	GATTTAAAGAATTCACCT a909_ail.seq
	T C A A A C A T T A C C A A A G C T T A T G C T G T A C C G T T T	GTGTTGGAATTACCAGT Majority
	2860 2870 2880	2890 2900
48 17	T C A A A C A T T A C C A A A G C T T A T G C T G T A C C G T T T	GTGTTGGAATTACCAGT 2603_ail.seg
49	T C A A A C A T T A C C A A A G C T T A T G C T G T A C C G T T T T C A A A C A T T A C C A A A G C T T A T G C T G T A C C G T T T	GTGTTGGAATTACCAGT 18rs21_a11.seq
49		C C T C T T C C A A T T A C C A C T AIRITH ALL AND
51	- I C A A A C A T T A C C A A A G C T T A T G C T G T A C C G T T T	GTGTTGGAATTACCACT nom216 ail com
50	T C A A A C A T T A C C A A A G C T T A T G C T G T A C C G T T T	GTGTTGGAATTACCAGT a909_ail.seq
	T G C T A A C T C T A C A G G T A C A G G T T T C C T T T C T G A	AATTAATATTTACCCTA Majority
	2910 2920 2930	2940 2950
98	TGCTAACTCTACAGGTACAGGTTTCCTTTCTGA	AATTAATATTACCCTA 2603_ail.seq
67 99	T G C T A A C T C T A C A G G T A C A G G T T T C C T T T C T G A T G C T A A C T C T A C A G G T A C A G G T T T C C T T T C T G A	AATTAATATTACCCTA 18rs21_a11.seq
39 .	- I G C T A A C T C T A C A G G T A C A G G T T T C C T T T C T C A	AATTAATATTACCCTA aibiii aii aan
)1	- IGUTAACICTACAGGTACAGGTTTCCTTTCTCA	AATTAATATTACCCTÁ manate att ann
ю	1 G C T A C T C T A C A G G T A C A G G T T T C C T T T C T G A	AATTAATATTACCCTA a909_ail.seq
	A A A A C G T T G T A A C T G A T G A A C C A A A A A C A G A T A	AAGATGTTAAAAAATTA Majority
	2960 2970 2980	2990 3000
8	A A A A C G T T G T A A C T G A T G A A C C A A A A A C A G A T A	AAGATGTTAAAAAATTA 2603_ail.seq
.7 9	A A A A C G T T G T A A C T G A T G A A C C A A A A A C A G A T A A A A A C G T T G T A A C T G A T G A A C C A A A A A C A G A T A	AAGATGTTAAAA AAATTA 18rs21_aii.seq
9	- A A A A C G T T G T A A C T G A T G A A C C A A A A A C A G A T A	AAGATGTTAAAAAATTA cibiii sii soo
ı	A A A A C G T T G T A A C T G A T G A A C C A A A A A C A G A T A	AAGATGTTAAAAAATTA nem316 ail see
0	A A A A C G T T G T A A C T G A T G A A C C A A A A A C A G A T A	A A G A T G T T A A A A A A T T A a909_ai1.seq
	G G T C A G G A C G A T G C A G G T T A T A C G A T T G G T G A A	GAATTCAAATGGTTCTT Majority
	3010 3020 3030	3040 3050
3	G G T C A G G A C G A T G C A G G T T A T A C G A T T G G T G A A	GAATTCAAATGGTTCTT 2603_ail.seq
7 9	G G T C A G G A C G A T G C A G G T T A T A C G A T T G G T G A A G G T C A G G T T A T A C G A T T G G T G A A	GAATTCAAATCCTT 18re21 211 coc
9	- GGTCAGGACGATGCAGGTTATACGATTGGTGAA	GAATTCAAATCCTTCTT olbiil out oog
1	- G G T C A G G A C G A T G C A G G T T A T A C G A T T G G T G A A.	GAATTCAAATCCTTCTT remain out ooc
)	G G T C A G G A C G A T G C A G G T T A T A C G A T T G G T G A A	GAATTCAAATGGTTCTT a909_aif.seq
	CAAATCTACAATCCCTGCCAATTTAGGTGACTA	T.G.A.A.A.A.T.T.G.A.A.A.T.T.A. Majority
	3060 3070 3080	3090 3100
8 7	GAAATCTACAATCCCTGCCAATTTAGGTGACTA GAAATCTACAATCCCTGCCAATTTAGGTGACTA	T G A A A A A T T T G A A A T T A 2603_ail.seq
. e	G	T G A A A A A T T T G A A A T T A coht att sea
ıs	- G A A A I U I A U A A I U C C I G C C A A I I I A G G I G A C I A	T C A A A A T T T C A A A T T A cititle and
4	TU A A A T C T A C A A T C C C T G C C A A T T T A G G T G A C T A .	T. C. A. A. A. A. T. T. T. C. A. A. T. T. A. mondate and
	GAAATCTACAATCCCTGCCAATTTAGGTGACTA	
•	CTGATAAATTTCCACATGCCTTGACTTATAAAT	
9ġ	3110 3120 3130 GTC ATA A A T T T C C A C A T C C C T T C A C A	3140 3150
7	C T G A T A A A T T T G C A G A T G G C T T G A C T T A T A A A T C T G A T A A A T T T G C A G A T G G C T T G A C T T A T A A A T	CTGTTGGAAAAATCAAG° 2603 ai1.seq
13.	CIGALAAATIIGCAGAIGGCTIGACTTATAAAT	CTGTTGGAAAAATCAAC cobt ail soc
9	CIGATAAATTTGCAGATGGCTTGACTTATAAAT	CTGTTGGAAAATCAAG cibiil ail sog
'1	CIGAIAAATTTGCAGATGGCTTGACTTATAAAT	CTGTTGGAAAAATCAAC pengi6 ail sog
•	CTGATAAATTTGCAGATGGCTTGACTTATAAAT	CTGTTGGAAAAATCAAG a909_a11.seq

3160 3180 3190 ATTGGTTCGAAAACACTGAATAGAGATGAGCACTACACTATTGATGAACC 2603_ai1.seq 148 ATTGGTTCGAAAACACTGAATAGAGATGAGCACTACTATTGATGAACC 18rs21_ai1.seq 917 149 A T T G G T T C G A A A C A C T G A A T A G A G A T G A G C A C T A C A C T A T T G A T G A A C C cohi_ail.seq ATTGGTTCGAAAACACTGAATAGAGATGAGCACTACAGTATTGATGAACC cjb111_ai1.seq ATTGGTTCGAAAACACTGAATAGAGATGAGCACTACACTATTGATGAACC nem316_ai1.seq ATTGGTTCGAAAACACTGAATAGAGACACTACACTATTGATGAACC a909_ail.seq AACAGTTGATAACCAAAATACATTAAAATTACGTTTAAACCAGAGAAAT Majority 3210 3220 3230 3240 3250 AACAGTTGATAACCAAAATACATTAAAATTACGTTTAAACCAGAGAAAT 2603_ai1.seq AACAGTTGAT,AACCAAAATACATTAAAATTACGTTTAAACCAGAGAAAT 18rs21_a11.seq 967 AACAGTTGATAACCAAAATACATTAAAATTACGTTTAAACCAGAGAAAT cohl_all.seq AACAGTTGATAACCAAAATACATTAAAATTACGTTTAAACCAGAGAAAT cjbiii_ai1.seq AACAGTTGATAACCAAAATACATTAAAAATTACGTTTAAACCAGAGAAAT nem316_aii.seq 102 AACAGTTGATAACCAAAATACATTAAAATTACGTTTAAACCAAGAAAT a909_ai1.seq TTAAAGAAATTGCTGAGCTACTTAAAGGAATGACCCTTGTTAAAAATCAA Majority 3260 3270 3280 3290 3300 248 TTAAAGAAATTGCTGAGCTACTTAAAGGAATGACCCTTGTTAAAAATCAA 2603_ai1.seq TTAAAGAAATTGCTGAGCTACTTAAAGGAATGACCCTTGTTAAAAATCAA 18rs21_ai1.seq 117 TTAAAGAAATTGCTGAGCTACTTAAAGGAATGACCCTTGTTAAAAATCAA cohlail.seq 249 TTAAAGAAATTGCTGAGCTACTTAAAGGAATGACCCTTGTTAAAAATCAA cjbiii_aii.seq 249 TTAAAGAAATTGCTGAGCTACTTAAAGGAATGACCCTTGTTAAAAATCAA nem316_ai1.seq TTAAAGAAATTGCTGAGCTACTTAAAGGAATGACCCTTGTTAAAAAATCAA a909_ail.seq GAT GCTCTTGATAAAGCTACTGCAAATACAGATGCTGCGCATTTTTGGA Majority 3320 3330 3340 3350 GATGCTCTTGATAAAGCTACTGCAAATACAGATGCGGCATTTTTTGGA 2603_ail.seq 298 GATGCTCTTGATAAAGCTACTGCAAATACAGATGCGGCATTTTTGGA 18rs21_ai1.seq **167** GATGCTCTTGATAAAGCTACTGCAAATACAGATGCCGGCATTTTTGGA cohl_ail.seq 199 GATGCTCTTGATAAACCTACTGCAAATACAGATGATGCGGCATTTTTGGA.cjb111_ai1.seq 199 GATGCTCTTGATAAACCTACTGCAAATACAGATGATCCGGCATTTTTCGA nem316_ail.seq IO1 GAT G C T C T T G A T A A A G C T A C T G C A A A T A C A G A T G C G G C A T T T T T G G A a909_ail.seq ATTCCAGTTGCATCAACTATTAATCAAAAGCAGTTTTAGGAAAAGCAA Majority 3360 3370 3380 3390 AATTCCACTTGCATCAACTATTAATGAAAAGCAGTTTTAGGAAAAGCAA 2603_ail.seq AATTCCAGTTGCATCAACTATTAATGAAAAGCAGTTTTAGGAAAAGCAA 18rs21_ai1.seq AATTCCAGTTGCATCAACTATTAATGAAAGCAGTTTTAGGAAAACCAA coh1_ai1.seq AATTCCAGTTGCATCAACTATTAATGAAAAGCAGTTTTAGGAAAAGCAA cjb111_a11.seq AATTCCAGTTGCATCAACTATTAATGAAAGCAGTTTTAGGAAAAGCAA nem316_ail.seq AATTCCAGTTGCATCAACTATTAATGAAAAGCAGTTTTAGGAAAAGCAA a909_ai1.seq TTGAAAATACTTTTGAACTTCAATATGACCATACTCCTGATAAAGCTGAC Majority 3410 3420 3430 3440 TTGAAAAATACTTTTGAACTTCAATATGACCATACTCCTGATAAAGCTGAC 2603_ail.seq 98 TTGAAAATACTTTTGAAGTTCAATATGACCCATACTCCTGATAAGCTGAC:18rs21 a11. seq TTGAAAATACTTTTGAACTTCAATATGACCTCCTGATAAGCTCAC contailseq TTGAAAATACTTTTGAACTTCAATATGACCATACTCCTGATAAAGCTGAC cibiii aili seq TTGAAAATACTTTTGAACTTCAATATCACCCCTCCTCATAAACCTCAC nem316 alk seq TTGAAAATACTTTGAACTTCAATATCACTCCTGATAAAGCTGAC a909_a414.seq AATECAAAACCATCTAATCCTCCAAGAAACCAACTTCATACTCCTGCTGC 3460 . 3470 3500 3490 AATCCAAAACCATCTAATCCTCCAAGAAACCAGAAGTTCATACTGGTGG 2603_ail.seq AATCCAAAACCATCTAATCCTCCAAGAAACCAGAAGTTCATAGTGGTGG 18rs21_ail.seq A A T C C A A A A C C A T C T A A T C C T C C A A G A A A A C C A G A A G T T C A T A C T G G T G G cohl_ail.seq AATCCAAAACCATCTAATCCTCCAAGAAACCAGAAGTTCATACTGGTGG cjb111_ai1.seq AATCCAAAACCATCTAATCCTCCAAGAAACCAGAAGTTCATACTGGTGG nem316_ai1.seq AATCCAAAACCATCTAATCCTCCAAGAAACCAGAAGTTCATACTGGTGG a909_a11.seq



-	CTGAC	A TO A C C G T T G A E	A.G. T. C. C. T. C. A. T. C. C.	///	<u>·</u>
		3860		AACACCTGAT	ACAATTAAAAAC Majority
3848	CTCAC		3870	3880	
3617	CTGAC	A I CACGGTTGAT A T CACGGTTCAT	AGTGCTGATGC	AACACCTGAT	TACAATTAAAAAC 2603_aii.seq
3849	CIGACI	ATCACCCTTCAT	10000000	O I G A I	A CARLLARARA C 18rc21 old man
3849	CIGACI	ATCACCCTTCAT	1 C T C C T C	O O Z G A I	A CARLLARARA C COM 311 con
3851	CIGACA	ATCACCCTTCAT	1050000	TOOLGYI	A CAALLAAAAA C cibiii ah aa
3850	CIGAC	A T C A C G G T T G A T	AGTGCTGATGC	AACACCTGAT	A C A A T T A A A A A C nem316_ail.seq A C A A T T A A A A A C a909_ail.seq
	A A C A A A	CCTCCTTCAAT			a o A A I I A A A A A C a909_all.seq
		2010	CCCTAATACTG	<u>G T G G T A T T G G</u>	TACCCTATCTT Majority
3898		0010	3920	3930	20.40
3667	AACAAA	CCTCCTTCAAT	CCCTAATACTG	GTGGTATTGG	
3899	AAUAAA	$\mathbf{C}\mathbf{G}\mathbf{T}\mathbf{C}\mathbf{C}\mathbf{T}\mathbf{T}\mathbf{C}\mathbf{A}\mathbf{A}\mathbf{T}$	C C C C C C C C C C C C C C C C C C C	o rootutiee	ACCCCTAT.CTT 18re21 211 00m
3899		. C.C.T.C.C.T.C.A.A.m.		T T T G G	LACEUTATETT contents
3901 3900		. C.C.T.C.C.T.T.C.A.A.T.		0 * 0 0 1 V 1 1 G G	I A C G G C T A T C T T cibit i dit com
3900	AACAAA	CGTCCTTCAAT	CCCTAATACTG	GTGGTATTGG	TACGGCTATCTT nem316_ai1.seq TACGGCTATCTT a909_ai1.seq
	TGTCGC	TATCGGTGCTC	CCTCLTCCT		ail.seq
		2000	SGIGATGGCT	TTTGCTGTTA	A G G G G A T G A A G C Majority
2040			3970	3980	2000
3948 3717	TGTCGC	TATCGGTGCTG	CGGTGATGGCT	TTTGCTGTTA	
3949	TGTCGC	TATCCCTCCTC	GGTGATGGCT	TTTGCTGTTA	A G G G G A T G A A G C 2603_a11.seq A G G G G A T G A A G C 18rs21_a11.seq
3949	16166	ΤΑΤΓΕΓΤΓΕΤΑ	1 0 0 m 0 4 · · · ·	o o r.G r r W	A G G G G G G G G G G G G G G G G G G G
3951	TGTCGC	ТАТСССТЕСТЕЛ	100 000	GO 1, G 1 1 K	A G G G G A T G A A G C CILITI ALL ALL
1950	TGTCGC	TATCGGTGCTGG	GGTGATGGCT	TTGCTGTTA	A G G G G A T G A A G C nem316_ai1.seq A G G G G A T G A A G C a909_ai1.seq
	G.T.C.G.T.A	CAAAACATAAG		O T G T L, A	A G G G A I G A A G C a909_ail.seq
	,	JAKAR GRIKACI	AAATAAAAGG	TACTTCTTA	A C T A A C C A T G T T Majority
2000		. 2020	4020	4030	10.10
1998 1767	GTCGTA	CAAAAGATAACT	AAATAAAAGG	TACTTCTTA	
1999	GTCGTA	CAAAACATAACT	11100	HOLLOILA	A G I A A C C A T G T T 18re21 ail con
1999	GICGIA	CAAAACATAACT	4 4 4 5 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	CIIA	" G LAAC CAT GTT cobt att com
LOO1	GFCGTA	CAAAACATAACT			* G I A A C C A T G T T cibiti air con
KOOO"	GICGTA	CAAAAGATAACT	AAATAAAGGC	TACTTCTTA	AGTAACCATGTT nem316_ail.seq AGTAACCATGTT a909_ail.seq
_	TAAGAAA	AAGAGAAATACC	CTT		seq. as o o n 1 o 1 1 as os_ail.seq
		4060			TTTAAAATAAA Majority
.048	TAACAA		4070	080	4090 4100
817	TAAGAAA	A A G A C A · A A T A C C	CTTATTTCTCT	TTTGTCGTT	TTTAAAATAA 2603_aii_seq
1049	LAAGAAA	LACACAAATACO	0 m m + = = = = = = = = = = = = = = = = =		I I I A A A A T A A A 18re21 211 con
049	I A A G A A A	ACACAAATAAA	0		A LAAAATAAA cobi aii coc
050	I A A G A A A	AGAGAAATAGC	CTTATTTCTCT	TTTTGTCGTT	TTTAAAATAAA cjb111_ail.seq TTTAAAATAAA nem316_ail.seq
ļ	•				I I I A A A A T A A A agog ail sec
٠ .	GGAACAT	CATGAAACAAA	CATTAAAACTT	1 T C'T T T T T T	TTCTCTTCATC Majority
		4110	4120	AIGIIIICTT	TTCTGTTGATG Majority
098	G GVA A CAT			130	140 4150
867	GGAACAT	CATGAAACAAA	CATTAAAACTT	ATGTTTTCTT	TTCTGTTGATG 2603_ai1.seq
099 (3 G.A.A.C A.T	CATCAAACAAA	O'v m m · · · · · · · · · · · · · · · · ·	************	1 LUTGTTGATG 18cs21 at 1 con
099 4	. GAACAT	CATCALACALA		War in a reserve of their	4 TUTGT GTTGATE CONTAIL CON
100 (GAACAT	CATGAAACAAA	CATTAAAACTT	ATGTTTCT	TTCTCTTCATC cjb141_ail_seq TTCTTCATC nem316_ail_seq
200	, o, a, a, c, a, i	GAAAACAAA	CATTAAAACTT	ATGTTTCTT	TTGTGTTGATG nem316_all.seq TTGTGTTGATG a909_all.seq
<u>1</u>	TAGGGA	CTATCTTTCCA	TTACCONALG		CAAGAAACTCA Majority
		4160			CAAGAAACTCA Wajority
148 7	TAGGG			80 4	190 4200
917 T	TAGGGA	CTATETTTCCA	TTAGCCAAAC	GTTTTAGEG	CAAGAAACTCA 2603_ai1.seq
149 . 1	TAGECL	TT ATT TT TT TO T			UAAGAACTCA 18-col ali a
149 - 1	IAGGGA	CTATCTTTCCAA	TT	···· · · · · · · · · · · · · · · · · ·	CAAGAACTCA coblisit con
191 1	TAGGGA	CTATCTTTCCAA	T T 4 0 0 0 1 1 1		UAAGAAACTCA cibiil ail coc
1	· n u u u A	O LATUTTT G G A A	TTAGCCAAAC	GTTTTAGCG	CAAGAAACTCA nem316_ai1.seq CAAGAAACTCA a909_ai1.seq
					urracq

CT/US2005/027239

Alignment Report of Al-1WO 2006/078318 nethod with Weighted residue weight table Thursday, July 29, 2004 5:46 PM TCAGTT CRECKTTE TELETICAL CALCGERATION TO ATCGTCCAAATC Majority 4210 4230 4240 4250 TCAGTTGACGATTGTTCATCTTGAAGCAAGGGATATTGATCGTCCAAATC 2603_ai1.seq TCAGTTGACGATTGTTCATCTTGAAGCAAGGGATATTGATCGTCCAAATC 18rs21_ai1.seq TCAGTTGACGATTGTTCATCTTGAAGCAAGGGATATTGATCGTCCAAATC cohl_ail.seq 4199 TCAGTTGACGATTGTTCATCTTGAAGCAAGGGATATTGATCGTCCAAATC cjbill_ail.seq 4199 TCAGTTGACGATTGTTCATCTTGAAGCAAGGGATATTGATCGTCCAAATC nem316_ai1.seq 4201 TCAGTTGACGATTGTTCATCTTGAAGCAAGGGATATTGATCGTCCAAATC a909_a11.seq 4200 CACAGTTGGAGATTGCCCCTAAAGGAAGGACTCCAATTGAAGGAGTACTC Majority 4260 4270 4280 4290 4300 CACAGTTGGAGATTGCCCCTAAAGAAGGGACTCCAATTGAAGGAGTACTC 2603_all.seq 4248 CACAGTTGGAGATTGCCCCCTAAAGGAAGGGACTCCAATTGAAGGAGTACTC 18rs21_a11.seq 4017 CACAGTTGGAGATTGCCCCTAAAGAAGGGACTCCAATTGAAGGAGTACTC cohi_all.seq CACAGTTGGAGATTGCCCCTAAAGAAGGGACTCCAATTGAAGGAGTACTC cjblll_all.seq 4249 1249 CACAGTTGGAGATTGCCCCTAAAGAAGGGACTCCAATTGAAGGAGTACTC nem316_a11.seq (251 CACAGTTGGAGATTGCCCCTAAAGAAGGGACTCCAATTGAAGGAGTACTC a909_ail.seg 1250 TATCAGTTGTACCAATTAAAATCAACTGAAGATGGCGATTTGTTGGCACA Majority 4310 4320 4330 4340 4350 TATCAGTTGTACCAATTAAAATCAACTGAAGATGGCGATTTGTTGGCACA 2603_ai1.seq 1298 TATCAGTTGTACCAATTAAAATCAACTGAAGATGGCGATTTGTTGGCACA 18rs21_ai1.seq 1067 TATCAGTTGTACCAATTAAAATCAACTGAAGATGGCGATTTGTTGGCACACohl_ail.seq 1299 TATCAGTTGTACCAATTAAAATCAACTGAAGATGGCGATTTGTTGGCACA cjbiii_aii.seq 1299 TATCAGTTGTACCAATTAAAATCAACTGAAGATGGCGATTTGTTGGCACA nem316_all.seq 1301 TATCAGTTGTACCAATTAAAATCAACTGAAGATGGCGATTTGTTGGCACA a909_ai1.seq 1300 TTGGAATTCCCTAACTATCACAGAATTGAAAAAACAGGCGCAGCAGTTT Majority 4360 4370 4380 4390 4400 TTGGAATTCCCTAACTATCACAGAATTGAAAAAACAGGCGCAGGTTT 2603_a11.seq 1348 TTGGAATTCCCTAACTATCACAGAATTGAAAAACAGGCGCAGCAGGTTT 18rs21_aii.seq 1117 TTGGAATTCCCTAACTATCACAGAATTGAAAAAACAGGCGCAGCAGGTTT cohl_ai1.seq 1349 TTGGAATTCCCTAACTATCACAGAATTGAAAAAACAGGCGCAGCAGGTTT cjb111_ai1.seq 1349 TTGGAATTCCCTAACTATCACAGAATTGAAAAAACAGGCGCAGCAGCAGGTTT nem316_ail.seq 1351 TTGGAATTCCCTAACTATCACAGAATTGAAAAAACAGGCGCACCAGGTTT a909_ai1.seq 1350 TTGAAGCCACTACTAATCAACAAGGAAAGCTACATTTAACCAACTACCA 4410 4420 4430 4440 4450 TTGAAGCCACTACTAATCAACAAGGAAAGGCTACATTTAACCAACTACCA 2603_ail.seq 398 TTGAAGCCACTACTAATCAACAAGGAAAGGCTACATTTAACCAACTACCA 18rs21_a11.seq 167 TTGAAGCCACTACTAATCAACAAGGCTACATTTAACCAACTACCA cohlail.seq 1399 TTGAAGCCACTACTAATCAACAAGGAAAGGCTACATTTAACCAACTACCA cjbli1_ai1.seq 399 TTGAAGCCACTACTAATCAACAAGGAAAGGCTACATTTAACCAACTACCA nem316_ai1.seq 401 TTGAAGCCACTACTAATCAACAAGGCTACATTTAACCAACTACCA a909_a11.seq 400 CATGGAATTTATTATGGTCTGGCGGTTAAAGCCGGTGAAAAAATCGTAA Majority 4460 4470 4480 4490 4500 GATGGAATTTATTATGGTCTGGCGGTTAAAGCCGGTGAAAAAACCGTAA 2603 all seq 448 GATGGAATTTATTATGGTCTGGCGTTAAAGCCGGTGAAAAAATCGTAA 18cs21 all seq 217 GATGGAATTTATTATCGTCTGGCGTTTAAAGCCCGGTGAAAAAATCGTAA cohlati.seq 449 449: GATCCAATTTATTATCCTCCCCTTAAACCCCCGTCAAAACCCCCGTAAAAACCCCAAAAAAACCCTAA nee316 all seq 451 450 GAPCCAATTTATTATCCTCCCCCTTAAACCCCGGTCAAAAATCGTAA agog ail seq TGTGTGAGCTTCTTGGTTGACTTGTCTGAGGATAAAGTGATTATGCTA 4510 4520 4530 4540 4550 TGTCTCAGCTTTCTTGGTTGACTTGTCTGAGGATAAAGTGATTTATCCTA 2603_aif.seq 498 TGTCTCAGCTTTCTTGGTTGACTTGTCTGAGGATAAAGTGATTTATCCTA-18rs21_ai1_seq TGTCTCAGCTTCTTGGTTGACTTGTCTGAGGATAAAGTGATTTATCCTA cohl_all.seq TGTCTCAGCTTTCTTGGTTGACTTGTCTGAGGATAAAGTGATTTATCCTA cjbiii_ai1.seq TGTCTCAGCTTTCTTGGTTGACTTGTCTGAGGATAAAGTGATTTATCCTA nein316_a11.seq

TGTCTCAGCTTCTTGGTTGACTTGTCTGAGGATAAAGTGATTTATCCTA a909_ail.seq

501

Alignment Report of At-1_WO 2006/078318 Thursday, July 29, 2004 5:46 PM CTCC ACA GET GA CTTCC ACTTCCTTAAAGTTGGTGGAT Majority AAATCATCE 4560 4580 4590 4600 AAATCATCTGGTCCACAGGTGAGTTGGACTTGCTTAAAGTTGGTGTGGAT 2603_ail.seq 4548 AAATCATCTGGTCCACAGGTGAGTTGGACTTGCTTAAAGTTGGTGTGGAT 18rs21_ai1.seq 4317 A A A T C A T C T G G T C C A C A G G T G A G T T G G A C T T G C T T A A A G T T G G T G T G G A T cohl_ail.seq 1549 AAATCATCTGGTCCACAGGTGAGTTGGACTTGCTTAAAGTTGGTGTGGAT cjbiii_aii.seq 4549 A A A T C A T C T G G T C C A C A G G T G A G T T G G A C T T G C T T A A A G T T G G T G T G C A T nem316_ai1.seq 4551 4550 A A A T C A T C T G G T C C A C A G G T G A G T T G G A C T T G C T T A A A G T T G G T G T G G A T a909_ail.seq G G T G A T A C C A A A A A A C C A C T A G C A G C C G T T G T C T T T G A A C T T T A T G A A A A Majority 4610 4620 4630 4640 4650 G G T G A T A C C A A A A A A C C A C T A G C A G G C G T T G T C T T T G A A C T T T A T G A A A A 2603_aii.seq 1598 G G T G A T A C C A A A A A A C C A C T A G C A G C C G T T G T C T T T G A A C T T T A T G A A A 18rs21_ail.seq 1367 G G T G A T A C C A A A A A C C A C T A G C A G G C G T T G T C T T T G A A C T T T A T G A A A A cohi_aii.seq 1599 1599 GGTGATACCAAAAACCACTAGCAGGCGTTGTCTTTGAACTTTATGAAAA cjbiil_ai1.seq GGTGATACCAAAAAACCACTAGCAGGCGTTGTCTTTGAACTTTATGAAA nem316_ail.seq 1601 G G T G A T A C C A A A A A A A C T A G C A G G C G T T G T C T T T G A A C T T T A T G A A A A a a 909_ail.seq 1600 GAATGGTAGGACTCCTATTCGTGTGAAAATGGGGTTCCATTCTCAAGATA Majority 4660 4680 4690 4700 1648 GAATGGTAGGACTCCTATTCGTGAAAAATGGGGTGCATTCTCAAGATA 2603_a11.seq GAATGGTAGGACTCCTATTCGTGTGAAAATGGGGTGCATTCTCAAGATA 18rs21_ai1.seq GAATGGTAGGACTCCTATTCGTGTGAAAATGGGGTGCATTCTCAAGATA cohl_ail.seq GAATGGTAGGACTCCTATTCGTGTGAAAATGGGGTGCATTCTCAAGATA cjbiii_aii.seq GAATGGTAGGACTCCTATTCGTGTGAAAATCGGGTGCATTCTCAAGATA nem316_ail.seq 1651 GAATGGTAGGACTCCTATTCGTGAAAAATGGGGTGCATTCTCAAGATA a909_aii.seq 1650 TTGACGCTGCAAAACATTTAGAAACAGATTCATCAGGGCATATCAGAATT Majority 4710 4720 4730 4740 4750 TTGACGCTGCAAAACATTTAGAAACAGTTCATCAGGGCATATCAGAATT 2603_ail.seq 1698 1467 TTGACGCTCCAAAACATTTAGAAACACTTCATCAGGGCATATCAGAATT 18rs21_ai1.seq TTGACGCTGCAAAACATTTAGAAACAGATTCATCAGGGCATATCAGAATT cohl_all.seq TTGACGCTGCAAAACATTTAGAAACAGATTCATCAGGGCATATCAGAATT cjb111_ai1.seq TTGACGCTGCAAAACATTTAGAAACAGATTCATCAGGGCCATATCAGAATT nem316_ail.seq. TTGACGCTGCAAAACATTTAGAAACAGATTCATCAGGGCATATCAGAATT a909_ail.seq TCCGGGCTCATCCATGGGGACTATGTCTTAAAAGAAATCGAGACACAGTC Majority 4760 4780 4790 4800 TCCGGGCTCATCCATGGGGACTATGTCTTAAAAGAATCGAGACACAGTC 2603_ail.seq 1748 TCCGGGCTCATCCATGGGGACTATGTCTTAAAAGAATCGAGACACAGTC 18rs21_xi1.seq TCCGGGCTCATCCATGGGGACTATGTCTTAAAAGAATCGAGACACAGTC cohl_ail.seq 1749 TCCGGGCTCATCCATGGGGACTATGTCTTAAAAGAATCGAGACACAGTC cjb111_ail.seq 1749 TCCGGGCTCATCCATGGGGACTATGTCTTAAAAGAATCGAGACACAGTC nem316_ai1.seq 1750 TCCGGGCTCATCCATGGGGACTATGTCTTAAAAGAATCGAGACACAGTC a909_aii.seq A G G A T A T C A G A T C G G A C A G G C A G A C T G C T G T G A C T A T T G A A A A A T C A A Majority 4810 4830 4840 ..4850 A G-G A T A T C A G A T C G G A C A G G C A G A G A C T G C T G T G A C T A T T G A A A A T C A A 2603 all seq AGGATATCAGATCGGACAGGCAGACACTGTGACTATTGAAAATCAA 18rs21 att.seq A G G A T A T C A G A T C G G A C A G G C A G A G A C T G C T G T G A C T A T T G A A A A T C A A cohl all seq A G.G A T.A.T.C.A.G A T.C.G.G.A.G.A.G.G.G.A.G.A.G.A.G.T.G.C.T.G.T.T.G.A.A.A.A.T.C.A.A. cjbill all seq 799 A G.C A.T. C. A. C. A. C. C. C. A. C. C. C. A. C. T. C. C. T. C. T. T. T. C. A. A. A. T. C. A. A. nem316_all_seq 1801 AGGATATOAGATEGGACAGGGAAGAGTGTGTGAGTATTGAAAAATCAA a909 all seq 1800 AAACAGTAACACTAACGATTGAAATAAAAATTCCGACACCTAAAGTG Majority 4860 4870 4880 4890 4900 AAA CAGTAACAGTAACGATTGAAAATAAAAAGTTCCGACACCTAAAGTG 2603_aii.seq 1848 AAACAGTAACAGTAACGATTGAAATAAAAATCTTCCGACACCTAAAGTG 18rs21_ai1.seq 617 849 A A A C A G T A A C A G T A A C G A T T G A A A A T A A A A A G T T C C G A C A C C T A A A G T G conil_ail.seq AAACAGTAACAGTAACGATTGAAAATAAAAAAGTTCCGACACCTAAAGTG cjb111_ai1.seq 849 AAACAGTAACAGTAACGATTGAAATAAAAAGTTCCGACACCTAAAGTG nem316_a11.seq 1851

1850

AAACAGTAACAGTAACGATTGAAAATAAAAGTTCCGACACCTAAAGTG a909_ai1.seq

WO 2006/078318

Alignment Report of Al-1_alignment, using J. Hein method with Weighted residue weight table. Thursday, July 29, 2004 5:46 P.M... TATTCCCAAAACAGGTGAGCAACAGGCAATGGC Majority CCATCTEGA GGACTCTT 4910 4920 4930 4940 4950 CCATCTCGAGGAGGTCTTATTCCCAAAACAGGTGAGCAACAGGCAATGGC 2603_ail.seq 4898 4667 CCATCTCGAGGAGGTCTTATTCCCAAAACAGGTGAGCAACAGGCAATGGC 18rs21_ai1.seq CCATCTCGAGGAGGTCTTATTCCCAAAACAGGTGAGCAACAGGCAATGGC cobi_aii.seq 4899 CCATCTCGAGGAGGTCTTATTCCCAAAACAGGTGAGCAACAGGCAATGGCCjbli1_ai1.seq 4899 CCATCTCGAGGAGGTCTTATTCCCAAAACAGGTGAGCAACAGGCAATGGC nem316_ail.seq 4901 CCATCTCGAGGAGGTCTTATTCCCAAAACAGGTGAGCAACAGGCAATGGC a909_ail.seq A C T T G T A A T T A T T C C T C C T A T T T T A A T T C C T T T A G C C T T A C G A T T A C T A T Majority 4960 4970 4980 4990 5000 ACTT GTAATT ATT GGT GGT ATTTTAATT GCT TTAGC CTTAC GATT ACTAT 2603_ail.seq 4948 ACTT GT AATT ATT GGT GGT ATTTT AATT GCT TT AGCCTT ACGATT ACT AT 18rs21_ai1.seq 4717 ACTTGTAATTGGTGGTATTTTAATTGCTTTAGCCTTACGATTACTAT cohl_a11.seq 4949 ACTTGTAATTATTGGTGGTATTTTAATTGCTTTAGCCTTACGATTACTAT cjbl11_ai1.seq 4949 ACTT GTAATTATT GGT GGT ATTTTAATT GCTTTAGCCTTACGATTACTAT nem316_a11.seq CAAAACATCGGAAACATCAAAATAAGGATTAGCATGGGACAAAAATCAAA Majority 5010 5020 5030 5050 5040 4998 CAAAACATCGGAAACATCAAAATAAGGATTAGCATGGGACAAAAATCAAA 2603_ail.seq CAAAACATCGGAAACATCAAAATAAGGATTAGCATGGGACAAAAATCAAA 18rs21_a11.seq 4767 CAAAACATCGGAAACATCAAAATAAGGATTAGCATGGGACAAAAATCAAA cohl_ail.seq CAAAACATCGGAAACATCAAAATAAGGATTAGCATGGGACAAAAATCAAA cjbiil_ail.seq 1999 5001 CAAAACATCGGAAACATCAAAATAAGGATTAGCATGGGACAAAAATCAAA nem316_a11.seq CAAAACATCGGAAACATCAAAATAAGGATTAGCATGGGACAAAAATCAAA a909_ai1.seq 5000 A A T A T C T C T A G C T A C G A A T A T T C G T A T A T G G A T T T T T C G T T T A A T T T T C T Majority . 5070 5080 5090 5100 AATATCTCTAGCTACGAATATTCGTATATGGATTTTTCGTTAATTTTCT 2603_ail.seq 5048 1817 AATATCTCTAGCTACGAATATTCGTATATGGATTTTTCGTTTAATTTTCT 18rs21_ail.seq AATATCTCTAGCTACGAATATTCGTATATGGATTTTTCGTTTAATTTTCT cohl_ail.seq 5049 5049 A A T A T C T C T A G C T A C G A A T A T T C G T A T A T G G A T T T T T C G T T T A A T T T T C T cjbiii_ai1.seq AATATCTCTAGCTACGAATATTCGTATATGGATTTTCGTTTAATTTCT nem316_a11.seq 5051 **50**50 A ATATCTCTAGCTACGAATATTCGTATATGGATTTTTCGTTTAATTTTCT a909_aii.seq TAGCGGGTTTCCTTGTTTTGGCATTTCCCATCGTTAGTCAGGTCATGTAC Majority 5110 5120 5130 **5140** 5150 TAGCGGGTTTCCTTGTTTTGGCATTTCCCATCGTTAGTCAGGTCATGTAC 2603_ai1.seq TAGCGGGTTTCCTTGTTTTGGCATTTCCCATCGTTAGTCAGGTCATGTAC 18rs21_ai1.seq TAGCGGGTTTCCTTGTTTTGGCATTTCCCATCGTTAGTCAGGTCATGTAC cohl_ai1.seq TAGCGGGTTTCCTTGTTTTGGCATTTCCCATCGTTAGTCAGGTCATGTAC cjbill_ail.seq TAGCGGGTTTCCTTGTTTTGCCATTTCCCATCGTTAGTCACGTCATGTAC ném316_ai1.seq TAGCGGGTTTCCTTGTTTTGGCATTTCCCATCGTTAGTCAGGTCATGTAC a909_all.seq TTTCAAGCCTCTCACGCCAATATTAATGCTTTTAAGAAGCTGTTACCAA Majority 5160 5170 5180 5190 5200 148 TTTCAAGCCTCTCACCCCAATATTAATGCTTTTAAAGAAGCTGTTACCAA 2603_a11.seq 917 TTTCAAGCCTCTCACGCCAATATTAATGCTTTTAAAGGAAGCTGTTACCAA 18rs21_ail.seq TTTCAAGCCTCTCACGCCAATATTAATGCTTTTAAAGAAGCTGTTACCAA cohlail.seq 149 TTTCAAGCCTCTCACCCCAATATTAATGCTTTTAAAGAAGCTCTTACCAA cjbiit aif seq 149 TIT CAAGCCTCTCACGCCAATATTAATGCTTTTAAAGCAAGCTGTTACCAA nee316 all seq 151 150 TTTCAAGCCTCTCACCCCAATATTAATCCTTTTAAACCAAGCTCTTACCAA a909 all seq GATTGACCGGGTGGATAATCGGCTTTAGAACTTGCTTATGCTTATA 5210 : 5220 5230 5240 5250 GATTGACCGGGTGGAGATTAATCGGCGTTTAGAACTTGCTTATGCTTATA. 2603_all.seq 198 GATTGACCGGGTGGAGATTAATCGGCGTTTAGAACTTGCTTATGCTTATA i8rs21_ai1.seq 967 GATTGACCGGGTGCACATTAATCCCCCTTTAGAACTTGCTTATGCTTATA cohlail.seq 199 GATTGACCGGGTGGAGATTAATCGGCGTTTAGAACTTGCTTATGCTTATAcjbii1_ai1_seq

GATTGACCGGGTGGAGATTAATCGGCGTTTAGAACTTGCTTATGCTTATA a909_aii.seq

Thursday, July 29, 2004 5:46 PM N. July 29, 2004 5:46 PM

ACGCCAGTATAGCAGGCTCCCAATATACTAATCCCAGCGCTTAAA Majority 5260 5280 5290 ACCCCAGTATACCAGCTCCAAAACTAATCCCAGCCCTTAAA 2603_all.seq 5248 ACGCCAGTATAGCAGGTGCCAAAACTAATGGCGAATATCCAGCGCTTAAA 18rs21_ai1.seq 5017 A C G.C C A G T A T A G C A G G T G C C A A A A C T A A T G G C G A A T A T C C A G C G C T T A A A cohi_aii.seq 5249 ACGCCAGTATAGCAGGTGCCAAAACTAATGGCGAATATCCAGCGCTTAAA cjbiii_ai1.seq 5249 ACGCCAGTATAGCAGGTGCCAAAACTAATGGCGAATATTCAGCGCTTAAA nem316_ai1.seq 5251 ACCCCAGTATACCAGGTCCAAAACTAATCCCAACCCATTAAA a909_ail.seq 5250 GACCCCTACTCTGCTGAACAAAGCAGGCAGGGTCGTTGAGTACGCCCG Majority 5310 5320 5330 5340 5298 GACCCCTACTCTGCTGAACAAAGCAGGCAGGGTCGTTGAGTACGCCCC 2603_ail.seq GACCCCTACTCTGCTGAACAAAGCAGGCAGGGGTCGTTGAGTA-CGCCCG 18rs21_a11.seq 5067 GACCCCTACTCTGCTGAACAAAGCAGGGGGGGGGTCGTTGAGTACGCCCG cohl_ail.seq 5299 GACCCCTACTCTGCTGAACA'AAAGCAGGCAGGGTCGTTGAGTACGCCCG cjb111_ai1.seq 5299 GACCCCTACTCTGCTGAACAAAGCAGGCAGGGGTCGTTGAGTACGCCCG nem316_aii.seq 5301 GACCCCTACTCTGCTGAACAAAGCAGGCAGGGGTCGTTGAGTACGCCCG a909_ail.seq 5300 CATGCTTGAAGTCAAAGAAAAAAATAGGTCATGTGATTATTCCAAGAATTA Majority 5360 5380 5390 CATGCTTGAAGTCAAAGAACAAATAGGTCATGTGATTATTCCAAGAATTA 2603_ai1.seq **i348** CATGCTTGAAGTCAAAGAACAAATAGGTCATGTGATTATTCCAAGAATTA 18rs21_ai1.seq CATGCTTGAAGTCAAAGAACAAATAGGTCATGTGATTATTCCAAGAATTA cohl_ai1.seq **i349** CATGCTTGAAGTCAAAGAACAAATAGGTCATGTGATTATTCCAAGAATTA cjbill_ail.seq CATGCTTGAAGTCAAAGAACAAATAGGTCATGTGATTATTCCAAGAATTA nen316_ail.seq CATGCTTGAAGTCAAACAAATAGGTCATGTGATTATTCCAAGAATTA a909_ai1.seq ATCAGGATATCCCTATTTACGCTGGCTCTGCTGAAGAAATCTTCAGAGG Majority 5430 5440 5450 ATCAGGATATCCCTATTTACGCTGGCTCTGCTGAAGAATCTTCAGAGC 2603_a11.seq ATCAGGATATCCCTATTTACGCTGGCTGTGAAGAAATCTTCAGAGG 18rs21_ai1.seq ATCAGGATATCCCTATTTACGCTGGCTCTGCTGAAGAAATCTTCAGAGG cohl ail.seq ATCAGGATATCCCTATTTACGCTGGCTCTGCTGAAGAAATCTTCAGAGG cjbl11_ai1.seq ATCAGGATATCCCTATTTACGCTGGCTGCTGAAGAAATCTTCAGAGG nem316_ai1.seq ATCAGGATATCCCTATTTACGCTGGCTGCTGAAGAAATCTTCAGAGG a909_ail.seq G G C G T T G G A C A T T T A G A G G G G A C C A G T C T T C C A G T C G T G G T G A G T C A A C Majority 5460 5480 5490 G G C G T T G G A C A T T T A G A G G G G A C C A G T C T T C C A G T G G T G G T G A G T C A A C 2603_ai1.seq 448 GGCGTTGGACATTTAGAGGGGACCAGTCTTCCAGTCGGTGGTGAGTCAAC 18rs21_ai1.seq 217 G G C G T T G G A C A T T T A G A G G G G A C C A G T C T T C C A G T C G G T G G T G A G T C A A C cohl_ail.seq 449 G G C G T T G G A C A T T T A G A G G G G A C C A G T C T T C C A G T C G T G G T G A G T C A A C cjbiii_aii.seq 449 451 GGCGTTGGACATTTAGAGGGGACCAGTCTTCCAGTCGGTGAGTCAAC nem316_aif.seq G G C G T T G G A C A T T T A G A C G G G A C C A G T C T T C C A G T C G G T G G T G A G T C A A C a909_aii.seq 450 TCATGCCGTTCTAACTGCCCATCGAGGGCTACCAACGGCCAAGCTATTTA Majority 5510 5520 5530 5540 5550 TCATGCCGTTCTAACTGCCGATCGAGGGCTACCAACGGCCAAGCTATTTA 2603_ai1.seq_. T C A T G C C G T T C T A A C T G C C C A T C G A G G G C T A C C A A C C G C C A A G C T A T T T A 18rs21_a11 seq T C A T G C C G T T C T A A C T G C C C A T C G A G G G C T A C C A A C G G C C A A G C T A T T T A cont. all. seq. TCATGCCGTTCTAACTGCCCATCGAGGGGCTACCAACGCCAAGCTATTTA cjbill ail seg TCATGCCGTTCTAACTGCCATCGAGGGGTACCAACGGCAAGGCAAGCTATTTA nem316 atl seq 501 TCATGCCGTTCTAACTGCCATCGAGGCTACGAACGCTATTTA agggail seq 500 CCAATTTAGACAAGGTAACAGTAGGTGACCGTTTTTACATTGAACACATC Majority 5560 5570 5580 5590 5600 C.C A A T T T A G A C A A G G T A A C A G T A G G T G A C C G T T T T T A C A T T G A A C A C A T C 2603_a11.seq 548 C.C.A.A.T.T.A.G.A.C.A.G.G.T.A.G.G.T.A.G.G.T.G.A.C.A.T.T.G.A.A.C.A.C.A.T.C. 18rs21_a11.seq CCAATTTAGACAAGGTAACAGTAGGTGACCGTTTTTACATTGAACACCCohl_ail.seq 549 CCAATTTAGACAAGGTAACAGTAGGTGACCGTTTTTACATTGAACACATCcjb111_a11.seq 549 C C A A T T T A G A C A A G G T A A C A G T A G G T G A C C G T T T T T A C A T T G A A C A C A T C nem316_at1.seq 551 CCAATTTAGACAAGGTAACAGTAGGTGACGGTTTTTACATTGAACACCATC a909_ail.seq

ilignment Report of Al-1_zangumeau, using J: Frem method with Weighted residue weight table. hursday, July 29, 2004 5:46 PM GGCGGAAATTATCGCCTGA Majority 5610 5620 5630 5640 G G C G G A A A G A T T G C T T A T C A G G T A G A C C A A A T C A A G T T A T C G C C C C T G A 2603_ail.seq G G C G G A A A G A T T G C T T A T C A G G T A G A C C A A A T C A A G T T A T C G C C C T G A 18rs21_a11.seq G G C G G A A A G A T T G C T T A T C A G G T A G A C C A A A T C A A A G T T A T C G C C C T G A coh1_ai1.seq GGCGGAAAGATTGCTTATCAGGTAGACCAAATCAAAGTTATCGCCCCTGA cjb111_a11.seq 601 G G C G G A A A G A T T G C T T A T C A G G T A G A C C A A A T C A A G T T A T C G C C C T G A nem316_a11.seq G G C G G A A A G A T T G C T T A T C A G G T A G A C C A A A T C A A A G T T A T C G C C C T C.A a909_al1.seq 600 T C A G T T A G A G G A T T T G T A C G T G A T T C A A G G A G A T C A C G T C A C C C T.A T Majority 5660 5670 5680 5690 5700 TCAGTTAGAGGATTTGTACGTGATTCAAGGAGAAGATCACGTCACCCTAT 2603_ail.seq 648 417 TCAGTTAGAGGATTTGTACCTGATTCAAGGAGAAGATCACGTCACCCTAT 18rs21_ai1.seq T C A G T T A G A G G A T T T G T A C G T G A T T C A A G G A G A T C A C G T C A C C C T A T cohl_all.seq 649 TCAGTTAGAGGATTTGTACCTGATTCAAGGAGATCACGTCACCCTAT cjb111_ai1.seq 649 T C A G T T A G A G G A T T T G T A C G T G A T T C A A G G A G A T C A C G T C A C C C T A T nem316_ai1.seq 651 650 T C A C T T A G A G G A T T T G T A C G T G A T T C A A G G A G A A G A T C A C G T C A C C C T A T a909_ail.seq TAACTT GCACACCTTATATGATAAGTCATCGCCTCCTCGTTCGAGGC Majority 5720 5730 5740 5750 698 TAACTTGCACACCTTATATGATAAATAGTCATCGCCTCCTCGTTCGAGGC 2603_ail.seq TAACTTGCACACCTTATATGATAAATAGTCATCGCCTCCTCGTTCGAGGC 18rs21_ai1.seq 467 TAACTTGCACACCTTATATGATAAATAGTCATCGCCTCCTCGTTCGAGGC cohl_ail.seq 599 TAACTTGCACACCTTATATGATAAATAGTCATCGCCTCCTTCGAGGC cjbii1_aii.seq 699 TAACTTGCACACCTTATATGATAAGTCATCCCTCCTCGTTCGAGGC nem316_ail.seq 701 TAACTT G CACACCT TATAT GATAAATAGT CATCGCCT CCTCGTT CGAGGC a909_ail.seq 700 A A G C G A A T T C C T T A T G T G G A A A A A A C A G T G C A G A A G A T T C A A A G A C C T T Majority 5760 5770 5780 5790 5800 AAGCGAATTCCTTATGTGGAAAAAACAGTGCAGAAAGATTCAAAGACCTT 2603_ai1.seq 748 AAGCGAATTCCTTATGTGGAAAAACAGTGCAGAAAGATTCAAAGACCTT 18rs21_ai1.seq 517 AAGCGAATTCCTTATGTGGAAAAACAGTGCAGAAAGATTCAAAGACCTT cohi_ai1.seq 749 AAGCGAATTCCTTATGTGGAAAAACAGTGCAGAAAGATTCAAAGACCTT cjb111_at1.seq 749 . AAGCGAATTCCTTATGTGGAAAAACAGTGCAGAAAGATTCAAAGACCTT nem316_ai1.seq 751 A A G C G A A T T C C T T A T G T G G A A A A A A C A G T G C A G A A A G A T T C A A A G A C C T T a909_a11.seq 750 CAGGCAACAACAATACCTAACCTATGCTATGTGGGTAGTCGTTGGACTTA Majority 5820 5830 5840 .5850 CAGGCAACAACAATACCTAACCTATGCTATGTGGGTAGTCGTTGGACTTA 2603_ail.seq 798 CAGGCAACAACAATACCTAACCTATGCTATGTGGGTAGTCGTTGGACTTA 18rs21_ai1.seq 567 CAGGCAACAACATACCTAACCTATCCTATGTGGGTACTCGTTGGACTTA cohl_ail.seq 799 CAGGCAACAACAATACCTAACCTATGCTATGTGGGTAGTCGTTGGACTTA cjb111_ai1.seq 799 CAGGCAACAACAATACCTAACCTATGCTATGTGGGTAGTCGTTGGACTTA nem316_ai1.seq 301 300 CAGGCAACAACAATACCTAACCTATGCTATGTGGGTAGTCGTTGGACTTA a909_a11.seq 5870 5880 · 5890 5900 TCTTGCTGTCGCTTCTCATTTGGTTTAAAAAGACAAAAAAAGCGGAAAAAAGCGGCGC2603_ai1.seq 14R · 317 149 149 TCTTCCTCCCCTTCTCATTTCCTTTAAAAACCCAAACACACAAAACCCCCDem316 all sen 151 TCTTGCTGTCCCTTCTCATTTGGTTTAAAAAGACGAAACAGAAAAGCGGGa909 antseq 150 A G A A G A A T G A A A A G C G G C T A G T C A A A A T A G T C A C A A T A A T T C G A A A T A Majority 5910 5920 5930 5940 5950 AGAAAGAATGAAAAGCCGGCTAGTCAAAATÁGTCACAATAATTCGAAATA-2603_ai1.seq AGAAAGAATGAAAAGCCGCTAGTCAAATAGTCACAATAATTCGAAATA 18rs21_ai1.seq 67 199 A G A A A G A A T G A A A A G C G G C T A G T C A A A A T A G T C A C A A T A A T T C G A A A T A coh1_a11.seq 199 AGAAAGAATGAAAAGCCGCTAGTCAAAATAGTCAAAATAGTCGAAATAcjb111_ail_seq AGAAAGAATGAAAAAGCCGGCTAGTCAAAATAGTCACAAATACTCGAAATA nem316_a11.seq 100

A G A A A G A A T G A A A A A G C G G C T A G T C A A A A T A G T C A C A A T A A T T C G A A A T A a909 all. seq

Thurs	Thursday, July 29, 2004 5:46 PM					
	ATAAAATEKT	ACCCTCATTI	T.G. C.A. T.G. G.G. A.G.T.C.	TGATTCTCTTATTT Majority		
	5960					
FO 40		00.0	5980	5990 6000		
5948	ATAAAATCAGA	ACCCTCATTTT	TGTGATGGGAAGTC	TGATTCTCTTATTT 2603_ail.seq		
5717	~	CAUCULUATTT	TGTGATGGGAACTC-	TO ATTOTOTATE TO ALL.	a	
5949	I A A A A I C A G A	A C C C I C A I I I I I	THI GATEGEAACTC	TC		
5949		LA C C C I C A T T T T	TETEATEGEAACTC	TCATTCTCTTITTT	a	
5951		A C C C I C A I I I I I		TC	a.	
5950	AIAAATCAGA	ACCCTCATTT	TGTGATGGGAAGTÇ	TGATTCTCTTATTT a909_ail.seq	•	
	CCGAIIGIGAG	CCAGGTAAGTT	A C T A C C T T G C T T C G C	CATCAAAATATTAA Majority		
	6010	6020	6030	6040 6050		
59 98	CCCATTCTCAC	C C A C C T A A C T T				
5767	CCGATTGTGAG	CCAGGIAAGII.	ACTACCTTGCTTCG	CATCAAAATATTAA 2603_ail.seq		
5999	CCGATTGTGAG	CCACCTAACTT	ACTACCTTCCTTCCT	CATCAAAATATTAA 18rs21_ai1.seq CATCAAAATATTAA coh1_ai1.seq	4	
5999	CCGATTGTGAG	CCACCTAACTT	ACTACCTTCCTTCC	CATCAAAATATTAA cohl_ail.seq CATCAAAATATTAA cjb111_ail.seq		
3001	CCGATTGTGAG	CCACCTAACTT	A C T A C C T T C C T T C C A	CATCAAAATATTAA cjbiii_aii.seq CATCAAAATATTAA nem316_aii.seq	1	
\$000	CCGATTGTGAG	CCAGGTAAGTT	ACTACCTTCCTTCC	CAICAAAA FATTAA nem316_all.seq CATCAAAATATTAA a909_all.seq	1	
-			. OI NOCII GCII CG (CAICAAAAAAAAAAa909_aii.seq		
	TCAATTTAAGC	GGGAAGTCGCT	AAGATTGATACTAAT	TACGGTTGAACGAC Majority		
			•	TACGOTT GAACGAC Majority		
	6060	6070	6080	6090 6100		
3048	TCAATTTAAGÇ	GGGAAGTCGCT	A.A.G.A.T.T.G.A.T.A.C.T.A.A.7	TACGGTTGAACGAC 2603_ail.seq		
,O.1.	IUNNIIINNEC		AAGATTGATACTAA1	T A C C C T T C A A C C A C 19-2111		
3049	IUMMILLARGO	GGGAAGTCGCT	AAGATTGATACTAAT	T A C C C T T C A A C C A C cold - 11	-	
3049	I CANIII AAGC	GGGAAGTCGCT	AAGATTGATACTAAT	TACCCTTC	3	
1051:	IUAALIIAAGU	GGGAAGTCGCT	AAGATTGATACTAAT	T A C C C T T C A A C C A C	;	
1050	ICAATTTAAGC	GGGAAGTCGCT	AAGATTGATACTAAT	TACGGTTGAACGAC nemsib_aii.seq	•	
				-		
	GORICGCI:II	GCIARIGCIIAC	CAATGAGACGTTATC	CAAGGAATCCCTTG Majority		
	6110	6120	6130	6140 6150		
i098	GCATCGCTTTA	GCTAATGCTTAG	CAATCACACCTTATC	CAAGGAATCCCTTG 2603_ail.seq		
i867	G C A I C G C.I I I A	GCTAATGCTTAC	CAATCACACCTTATC	C A A C C A A T C C C T T C 1021 - 11	_	
1099	GUNIUUULLIA	GCTAATGCTTAC	CAATGAGACGTTAT <i>C</i>	CAACCAATCCCTTC oobi air a	_	
1099	COLICULIA	GUIAATGUTTAO	CAATGAGACGTTATO	C		
1101	GCKICGCILIA	GULAATGUTTA(CAATGAGACGTTATC	CAACCAATCCCTTC momotic at and	i	
:100	G CATCGCTTTA	G-C T A A T G C T T A C	CAATGAGACGTȚATC	CAAGGAATCCCTTG headsto_att.seq.	,	
		•		•		
•		IIIIACCAGIAA	AGCAAAAGAAGGTT	TTGAGAGAGTATGC. Majority	•	
	6160	6170	6180	6190 6200		
148	CTTATAGACCC.	TTTTACCAGTAA	AGCAAAAGAAGGTT	TTGAGAGAGTATGC 2603_ail.seq		
917	CILKIAGACCC	IIITACCAGTAA	AGCAAAAAGAACCTT	PTCACACACTATCC 10-21 -11		
149	CITALAGACCC	TTTTACCAGTAA	AGCAAAAAGAACCTT	PTCACACACTATCC asks at a second		
149	CLIALAGACCC	I I I T A C C A G T A A	AGCAAAAAGAACCTT	FT G A C A C A C T A T C C - 15-111 - 11		
151	CITALAGACCC	TITTACCAGTAA	AGCAAAAAGAACCTT	TTGAGAGAGTATCC		
150	C T T A T A G A C C C	TTTACCAGTAA	A G C A A A A A G A A G G T T	TTGAGAGAGTATGC agog_ai1.seq		
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	I CGIAIGCIIG.	AAGITCATGAGC	<u> A A A T A G G T C A T G T G</u>	GCAATCCCAAGTA Majority		
:		6220	6230	6240 6250		
198	TCGTATCCTTC	AACTTCATCACC	CAAATACCTCATO	G C A A T C C C A A G T A 2603_ail_seq		
967	TCGTATGCTTG	AAGTTCLITCACC		GCAATCCCAAGTA 2603 ail seq GCAATCCCAAGTA 18rs21 ail seq		
199	TCGTATCCTTC	AAGTTCATCACC		G C A A T C C G A A G T A coht_all_seq		
199	TCGTATCCTTC	AAGTTCATGAGG	CAAATACCTCATOTC	GCAATGCCAAGTA contail seq		
ζŲ1	- L C G I A I G C 1:1, G.,	A A G T E C A T G A G C	C.A.A.A.T.A.G.G.T.G.A.T.G.T.C	C.C. G.A. T. C.O. C.A. A.O. T.A. Allega C. L. L.	=	
200	TEGTATECTE	AAGTTCATGAGE	AAATAGGTCATGTG	GCAATCCCAACTA a909_a11.seq	4	
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	TTCCCCTTCAT	ATTECAATTTAT	GCTGCAACATCCGA	AACTCTCTCAC Najority	•	
	6260	6270	6280	6290 6300		
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D17	TECCETTEAT	A I I U U A A T T T A T A T T C C A 4 T T T T 4 T	L G U.T G G A A C A T C C G A	AACTCTCTCAC 2603 all seq		
249	TTGGGGTTGAT	A T T C C & A T T T A T	I G C T C C A A C A T C C G A	A A C T G T G C T T C A G 18rs21 all seq		
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251	TTGGGGTTGAT	ATTCCAATTTAT	C C T C C A A C A T C C C A	AACTGTGCTTCAG cjbiii_aii.seq AACTGTGCTTCAG nem316_aii.seq		
250	TTGGGGTTGAT	ATTCCAATTTAT	CCTCCAACATCCCA	AACTGTGCTTCAG nem316_all.seq AACTGTGCTTCAG a909_all.seq		
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age 19

Thurs	day, July 29, 2004 5:46 PM		word abset	
	AAAGGTAGTGGGGAT	TI GG A GG G'AIA CO	ACTOTTCCAGTGGGAG	GTTTGTC Majority
	6310	6320	6330 . 6340	• · · · · · · · · · · · · · · · · · · ·
6298	AAAGGTAGTGGGAT	•		6350
6067	AAAGGTAGTGGGCAT	TTCCACCCAACC	AGTCTTCCAGTGGGAG	GTTTGTC 2603_ai1.seq
6299			AGTCTTCCAGTGGGAG	
6299				
6301				
6300	AAAGGTAGTCGCAT	TTGGAGGGAACC	AGTCTTCCAGTGGGAG	GTTTGTC agon att seq
	RACCCATICAGIACT	AACTGCCCACCG	TGGCTTGCCAACAGCT	A G G C T A T Majority
	. 6360	6370	6380 6390	6400
6348	AACCCATTCAGTACT	AACTGCCCACCC	TGGCTTGCCAACAGCT	
6117				
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6349 6351				
6350				
0000	and the restriction of the state of the stat	A W C I G C C C A G C G	TGGCTTGCCAACAGCTA	AGGCTAT a909_ail.seq
	TTACCGACTTAAATA	AAGTTAAAAAAC	GCCAGATTTTCTATGTC	
			•	ACGAAC Majority
	6410	6420	6430 6440	6450
6398	TTACCGACTTAAATA	AAGTTAAAAAAG	GCCAGATTTTCTATGT	A C G A A C 2603 att sen
6167 6399				
6399	noodaciinaai.	A A G I I A A A A A A C		
6401	TTACCGACTTAAATA	AAGIIAAAAAAG AAGTTAAAAAA	G C C A G A T T T T C T A T G T G G C C A G A T T T T C T A T G T G	ACGAAC cjbiii_aii.seq
6400	TTACCGACTTAAATA	AAGTTAAAAAAG	GCCAGATTTTCTATGTC	ACGAAC nem316_ail.seq
		•	•	
	ATCAAGGAAACACTT	CCCTACAAAGTC	G T G T C T A T C A A G T T G T	GGATCC Majority
	6460	6470	6480 6490	• •
6448	ATCAACCAAACACTT	CCCTACAAAA		6500
6217	ATCAAGGAAACACTT	G C C T A C A A A G T C	G T G T C T A T C A A A G T T G T G T G T C T A T C A A A G T T G T	G G A T C C 2603_ail.seq
6449				
5449				
6451 6450				
6450	AICARGGAAACACATT	GCCTACAAAGTC	GTGTCTATCAAAGTTGT	GGATCC a909_all:seq
	•		CAATGGTAAGGATTATA	
				TAACCT Majority
	6510	6520	6530 6540	6550
5498	AACAGCTTTAAGTGAG	GGTTAAGATTGT	CAATGGTAAGGATTATA	TAACCT 2603 all seg
5267 5499				
3499				
3501			C A A T G G T A A G G A T T A T A C A A T G G T A A G G A T T A T A	
3500	AACAGCTTTAAGTGAG	GTTAAGATTGT	C A A T G G T A A G G A T T A T A	TAACCT nem316_ail.seq
				-
	TGCTGACTTGCACACC	TTACATCA TCA	AT A.G.T.C.A.T.C.G.T.C.T.T.G	G T A A A A Majority
•	6560	6570	6590 6590	6600
i548 :	TGCTGACTCCACACC	TTACATO		9000
			A TAGTCATCGTCTCTTG	
1550	TGCTGACTTGCACACC	TTACATGATCA	TACTCATCGTCTCTTG	G T A A A a a a a a a a a a a a a a
		744		
		A L G A T L C T A C C C	A G G C G G A A A A G C A C A A	A G A A C A Majority
•	6610	6620	6630 6640	6650
1598	GGAGAGCGTATTCCTT	ATGATTCTACCO	A G G C G G A A A A G C A C A A	1.0.4.1:04.0000
367				
599				
599 601				
	a o k o o o i w i i c c i i	A T G A T T C. I A C C C	A G G C G G A A A G C A C A A	AGAACA a909_ail.seq
	a.			

Thursday, July 29, 2004 5:46 PM AACCGT ACAA ATTATCCT TTC FCACTACTGTTGAAGATACTACTAGTAT Majority 6660 6670 6680 6690 6700 AACCGTACAAGATTATCGTTTGTCACTAGTGTTGAAGATACTAGTAT 2603_ai1.seq 648 AACCGTACAAGATTATCGTTTGTCACTAGTGTTGAAGATACTACTAGTAT 18rs21_ai1.seq 1417 AACCGTACAAGATTATCGTTTGTCACTAGTGTTGAAGATACTAGTAT cohi_ail.seq 649 AACCGTACAAGATTATCGTTTGTCACTAGTGTCAAGATACTACTAGTAT cjbiii_ail.seq 649 AACCCTACAAGATTATCGTTTGTCACTAGTTTGAAGATACTACTAGTAT nem316_ail.seq 651 AACCGTACAAGATTATCGTTTGTCACTAGTGTTGAAGATACTACTAGTAT a909_ail.seq 650 6710 6720 6730 6740 6750 698 467 699 699 701 700 CGTCAATAACGATGTTGTGAATGGCTTACTTATCAAATAGGTGACT Majority 6760 6770 6780 6790 6800 748 CGTCAATAACGATGTTGTGAATGGCTTACTT ATCAAATAGGTGACT 2603_ail.seq CGTCAATAACGATGTTGTGAATGGCTTACTTATCAAATAGGTGACT 18rs21_ail.seq CGTCAATAACGATGTTGTGAATGGCTTACTTACTTATCAAATAGGTGACT coh1_a11.seq 749 CGTCAATAACGATGTTGTGAATGGCTTACTTACTTATCAAATAGGTGACT cjb111_ai1.seq 749 CCTCAATAACGATGTTGTGAATGGCTTACTTACTTATCAAATAGGTGACT nem316_ai1.seq 750 CGTCAATAACGATGTTGTGAATGGCTTACTTACTTATCAAATAGGTGACT a909_a11.seq AATGATGATTGTGAATAATGGTTATCTAGAAGGGAAAAAATGAAAAAA GA Majority 6810 6820 6840 6850 AATGATGATGTGAATAATGGTTATCTAGAAGGGGAGAAAATGAAAAGA 2603_a11.seq 794 AATGATGATGTGAATAATGGTTATCTAGAAGGGAAAAATGAAAAGA 18rs21_al1.seq AATGATGATTGTGAATAATGGTTATCTAGAAGGGAAAAAATGAAAAAGA cohl_ai1.seq 799 AATGATGATTGTGAATAATGGTTATCTAGAAGGGAAAAATGAAAAAGA cjbiii_aii.seq **799** . ROI ROO GACAAAAAATATGGAGAGGGTTATCAGTTACTAATCCTGTCCCAA Majority 6860 6870 6880 6890 -6900 GACAAAAATATGGAGAGGGTTATCAGTTACTTACTAATCCTGTCCCAA 2603_ai1.seq 344 GACAAAAAATATGGAGAGGGTTATCAGTTACTTACTAATCCTGTCCCAA 18rs21_ai1.seq 317 GACAAAAATATGGAGAGGGTTATCAGTTACTTACTAATCCTGTCCCAA cohl_ail.seq 349 GACAAAAAATATGGAGAGGGTTATCAGTTACTTACTAATCCTGTCCCAA cjblii_ai1.seq 349 GACAAAAATATGGAGAGGGTTATCAGTTACTTACTAATCCTGTCCCAA nem316_ai1.seq 351 GACAAAAATATGGAGAGGGTTATCAGTTACTTACTAATCCTGTCCCAA a909_aii.seq 350 ATT CCATT TGGTATATT GGT ACAAGGT GAAACCCAAGAT ACCAATCAAGC Majority 6910 6920 6930 6940 6950 ATTCCATTTCGTATATTCGTACAAGGTGAAACCCAAGATACCAATCAAGC 2603_all.seq 394 **67** ATTCCATTCGTATATTCGTACAAGGTGAAACCCAAGATCAAGC conlail.seq 399 ATT CCATTT GGTATATT CGTACAAGGTGAAACCCAAGATACCAATCAAGC cjb111 a11.seg 199. Ю1-000 6970 .6980 6990 7000 :: 144 ACTTGGAAAAGTAATTGTTAAAAAAACGGGAGACAATGCTACACCATTAG. 2603_aii.seq 117: ACTTGGAAAAGTAATTGTTAAAAAAACGGGAGACAATGCTACACATTAG 18rs21_a11.seq ACTTGGAAAAGTAATTGTTAAAAAAACGGGAGACAATGCTACACCATTAG cohi_ail.seq 149 149 ACTTGGAAAAGTAATTGTTAAAAAAACGGGAGACAATGCTACACCATTAG cjb111_ai1.seq ACTTGGAAAAGTAATTGTTAAAAAACGGGAGACAATGCTACACATTAG nem316_a11.seq 151

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ay, July 29, 2004 5 46 PM 7010 7020 7030 7040 7050 GCAAAGCGACTTTTGTGTTAAAAATGACAATGATAAGTCAGAAACAAGT 2603_ait.seq 5994 GCAAAGCGACTTTTGTGTTTAAAAATGACAATGATAAGTCAGAAACAAGT 18rs21_ai1.seq 3767 GCAAAGCGACTTTTGTGTTAAAAATGACAATGATAAGTCAGAAACAAGT cohl_aii.seq 5999 GCAAAGCGACTTTGTGTTAAAAATGACAATGATAAGTCAGAAACAAGT cjb111_ai1.seq 3999 GCAAAGCGACTTTGTGTTAAAAATGACAATGATAAGTCAGAAACAAGT nem316_ai1.seq 700 t G C A A A G C G A C T T T T G T G T T A A A A A T G A C A A T G A T A A G T C A G A A C A A G T a909_aii.seq 7000 CACGAAACGGTAGAGGGTTCTGGAGAAGCATTTGAAAACATAAACC Majority 7060 7070 7080 7090 7100 CACGAAACGTAGAGGGTTCTGGAGAAGCATTGAAAAACC 2603_ail.seq 7044 CACGAAACGGTAGAGGGTTCTGGAGAAGCAACCTTTGAAAACATAAACC 18rs21_a11.seq 3817 CACGAAACGCTAGAGGCTTCTGGAGAAGCATTGAAAACATAAACC cohl_ail.seq 7049 CACGAAACGGTAGAGGGTTCTGGAGAAGCAACCTTTGAAAACATAAAACC cjbiii_aii.seq 7049 CACGAAACGGTAGAGGGTTCTGGAGAAGCAACGTTTGAAAACATAAAACC nem316_a11.seq 705 L CACGAAACGGTAGAGGGTTCTGGAAAGCATTTGAAAACATAAACC a909_ail.seq 7050 T G G A G A C T A C A C A T T A A G A G A A G A A A C A G C A C C A A T T G G T T A T A A A A A A Majority 7110 7120 7130 . 7140 7150 TGGAGACTACACATTAAGAGAAAAAACAGCACCAATTGGTTATAAAAAAA 2603_ai1.seq 7094 TGGAGACTACACATTAAGAGAAACAGCACCAATTGGTTATAAAAAAAChlail.seq TGGAGACTACACATTAAGAGAAGAACAGCACCAATTGGTTATAAAAAA cjbii1_aii.seq TGGAGACTACACATTAAGAGAAACAGCACCAATTGGTTATAAAAAA nem316_ai1.seq /101 TGGAGACTACACATTAAGAGAAGAACAGCACCAATTGGTTATAAAAA a909_ail.seq CTGATAAAACCTGGAAAGTTAAAGTTGCAGATAACGGAGCAACAATAATC Majority 7160 7170 7180 7190 CTGATAAAACCTGGAAAGTTAAAGTTGCAGATAACGGAGCAACAATAATC 2603_ai1.seq **1144** CTGATAAAACCTGGAAAGTTAAAGTTGCAGATAACGGAACAATAATC 18rs21_ai1.seq 3917 CTGATAAACCTGGAAAGTTAAAGTTGCAGATAACGGAGCAACAATAATC cohlail.seq 1149 CTGATAAACCTGGAAAGTTAAAGTTGCAGATAACGGAGCAACAATAATC cjbiii_aii.seq CTGATAAAACCTGGAAAGTTAAAGTTGCAGATAACGGAGCAACAATAATC nem316_a11.seq CTGATAAACCTGGAAAGTTAAAGTTGCAGATAACGGAACAATAATC a909_ai1.seq GAGGGTATGGATGCAGATAAAGCAGAAACGAAAAGAAGTTTTGAATGC Majority 7210 7220 7230 7240 7250 GAGGGTATGGATGCAGATAAAGCAAGAAAGAAAGAAGTTTTGAATGC 2603_a11.seq. 1194 GAGGGTATGGATGCAGATAAAGCAGAAACGAAAAGAAGTTTTGAATGC 18rs21_ai1.seq 1967 7199 GAGGGTATGGATGCAGATAAAGCAGAAACGAAAAGAAGTTTTGAATGC coh1_ai1.seq GAGGGTATGGATGCAGATAAAGCAGAAACGAAAAGAAGTTTTGAATGC cjbiil_ail.seq 1199 /201 GAGGGTATGGATGCAGATAAAGCAGAAACGAAAAGAAGTTTTGAATGC nem316_ai1.seq GAGGGTATGGATGCAGATAAAGCAGAAACGAAAAGAAGTTTTGAATGC a909_ai1.seq 1200 CCAATATCCAAAATCAGCTATTTATGAGGATACAAAAGAAATTACCCAT Majority 7260 7270 7280 7290 7300 CCAATATCCAAAATCACCTATTTATCAGGATACAAAAGAAATTACCCAT 2603_all.seq CCAATATCCAAAATCAGCTATTTATCAGGATACAAAAGAAATTACCCAT. 18gs21_aii.seq CCAATATCCAAAATCACCTATTTATCACGATACAAAAGAAATTACCCAT contail seq CCAATATCCAAAATCAGCTATTTATCACGATACAAAGAAATTACCCAT cibiil ail seq 249 C.C.A.A.T.A.T.C.C.A.A.A.T.C.A.C.C.T.A.T.T.A.T.G.A.C.G.A.T.A.C.A.A.A.G.A.A.A.T.T.A.C.C.C.A.T. men316_ail.seq C C A A T A T C C A A A A T C A G C T A T T T A T G A G G A T A C A A A G A A A T T A C C C A T asog att. seq. TAGTTAATGTAGAGGGTTCCAAAGTTGGTGAACAATACAAAGCATTGAAT Majority 7310 7320 ... 7330 -7340 7350 TAGTTAATGTAGGGGTTCCAAAGTTGGTGAACAATACAAAGCATTGAAT 2603_a11.seq 294 TAGTTAATGTAGAGGGTTCCAAAGTTGGTGAACAATACAAAGCATTGAAT 18rs21_ai1.seq TAGTTAATGTAGAGGGTTCCAAAGTTGGTGAACAATACAAAGCATTGAAT coh1_ai1.seq 067 1299 1299 TAGTTAATGTAGAGGGTTCCAAAGTTGGTAACAATACAAAGCATTGAAT.cjbii1_ai1.seq TAGTTAATGTAGAGGGTTCCAAAGTTGGTAACAATACAATAGAAT nem316_ai1.seq 1301 TAGTTAATGTAGAGGGTTCCAAAGTTGGTGAACAATACAAAGCATTGAAT a909_a11.seq 7300

ay, July 29, 2004 5:46 PM CCAATAANA L.C. CA'A A A CATECT C'C'A A C'A CATTCCT GAACCTTGGTTATC Majority 7370 7380 7390 7400 7344 7349 CCAATAAATGGAAAAGATGGTCGAAGAGAGATTGCT.GAAGGTTGGTTATC cjb111_ai1.seq A A A A A A A T T A C A G G G G T C A A T G A T C T C G A T A A G A A T A A A T A T A A A A T T G Majority 7410 7420 7430 7440 7450 AAAAAAATTACAGGGGTCAATGATCTCGATAAGAATAAAAATTG 2603_ail.seq 7394 AAAAAAATTACAGGGGTCAATGATCTCGATAAGAATAAAATATC 18rs21_ai1.seq **1167** AAAAAAAAATACAGGGGTCAATGATCTCGATAAGAATAAAAATTG coh1_a11.seq AAAAAAATTACAGGGGTCAATGATCTCGATAAGAATAAAAATTC cjb111_a11.seq AAAAAAATTACAGGGGTCAATGATCTCGATAAGAATAAAAATTG nem316_aii.seq A A T T A A C T G T T G A G G G T A A A A C C A C T G T T G A A A C G A A G A A C T T A A T C A A Majority 7470 7480 7490 7500 AATTAACTGTTGAGGGTAAAACCACTGTTGAAACGAAAGAACTTAATCAA 2603_aii.seq 444 AATTAACTGTTGAGGGTAAAACCACTGTTGAAACGAAAGAACTTAATCAA 18rs21_a11.seq 217 449 AATTAACTGTTGAGGGTAAAACCACTGTTGAAACGAAAGTAATCAA cohl_ail.seq AATTAACTGTTGAGGGTAAAACCACTGTTGAAACGAAAGTAATCAA cjbii1_ai1.seq 449 AATTAACTGTTGAGGGTAAAACCACTGTTGAAACGAAGTTAATCAA nem316_at1.seq 451 AATTAACTGTTGAGGGTAAAACCACTGTTGAAACGAAAGTAATCAA a909_ail.seq 450 CCACTAGATGTCGTTGTGCTATTAGATAGTTCAAATAGTATGAATAATGA Majority 7510 7520 7530 7540 7550 CCACTAGATGTCGTTGTGCTATTAGATAATTCAAATAGTATGAATAATGA 2603_ai1.seq 494 CCACTAGATGTCGTTGTGCTATTAGATACTTCAAATAGTATGAATAATGA 18rs21_ai1.seq 267 CCACTAGATGTCGTTGTGCTATTAGATAATTCAAATAGTATGAATAATGA cohlail.seq 499 CCACTAGATGTCGTTGTGCTATTAGATAGTTCAAATAGTATGAATAATGA cjbiil ail.seq 499 CCACTAGATGTCGTTGTGCTATTAGATAATTCAAATAGTATGAATAATGA nem316_ai1.seq 501 CCACTAGATGTCGTTGTGCTATTAGATACTTCAAATAGTATGAATAATGA a909_ail.seq AAGAGCCAATAATTCTCAAAGAGCATTAAAAGCTGGGGAAGCAGTTGAAA Majority 7570 7580 7590 7600 AAGAGCCAATAATTCTCAAAGAGCATTAAAAGCTGGGAAGCAGTTGAAA 2603_ai1.seq 544 317 AAGAGCCAATAATTCTCAAAGAGCATTAAAAGCTGGGGAAGCAGTTGAAA 18rs21_ai1.seq AAGAGCCAATAATTCTCAAAGAGCATTAAAAGCTGGGGAAGCAGTTGAAAACh1_ai1.seq 549 AAGAGCCAATAATTCTCAAAGAGCATTAAAAGCTGGGGAAGCAGTTGAAA cjb111_a11.seq AAGAGCCAATAATTCTCAAAGAGCATTAAAAGCTGGGGAAGCAGTTGAAA nem316_ai1.seq 551 AAGAGCCAATAATTCTCAAAGAGCATTAAAAGCTGGGGAAGCAGTTGAAA a909_ail_seq A G C T G A T T G A T A A A A T T A C A T C A A A T A A A G A C A A T A G A GTAGCTCTTGTG Majority 7620 7630 7640 7650 A G C T G A T T G A T A A A A T T A C A T C A A A T A A A G A C A A T A G A G T A G C T C T T G T G 2603_a11.seq A G C T G A T T G A T A A A A T T A C A T C A A A T A A G A C A A T A G A C T A G C T C T T G T C 18rs21 at seq 367 AGCTGATTGATAAAATTACATCAAATAAAGACAATAGAGTAGCTCTTGTG cohl ail seq 599 A G C T G A T T G A T A A A A T T A C A T G A A A T A A A G A C A A T A G A G T A G G T C T T G T G cibiti att. seq 599 AGCTGATTGATAAAATTACATCAAATAAAGACAATAGACTAGCTCTTGTG ag00 all seq A C A T A T G C C T C A A C C A T T T T T G A T G G T A C T G A A G C G A C C G T A T G A A A G G G Wajority 7660 . 7670 7680 7690 A.CATATGCCTCAACCATTTTTGATGGTACTGAAGCGGACCGTATCAAAGGG 2603_ail.seq 644 ACATATGCCTCAACCATTTTTGATGGTACTGAAGCGACCGTATCAAAGGG 18rs21_ai1.seq 417 ACATATGCCTCAACCATTTTTGATGGTACTGAAGCGACCGTATCAAAGGG contail seq 649 A CATAT G C C T C A A C C A T T T T T G A T G G T A C T G A A G C G A C C G T A T C A A A G G G cjbiii_aii.seq. ACATATGCCTCAACCATTTTTGATGGTACTGAAGCGACCGTATCAAAGGG nem316_ai1.seq 550 . A C A T A T G C C T C A A C C A T T T T T G A T G G T A C T G A A G C G A C C G T A T C A A A G G G a909_ail.seq

WO 2006/078318

Vignment Report of Al-1_augument, using J. Frein method with Weighted residue w T/US2005/027239 hursday, July 29, 2004 5:46 PM 7710 7720 7730 7740 ACTTGCCGATCAAAATGGTAAAGCCCCTGAATGATAGTGTATCATGGGATT 2603_aii.seq A G T T G C C G A T C A A A A T G G T A A A G C G C T G A A T G A T A G T G T A T C A T G G G A T T 18rs21_ai1.seq 1467. AGTTGCCGATCAAAATGGTAAAGCGCTGAATGATAGTGTATCATGGGATT cohl_ail.seq 1699 AGTTGCCGATCAAAATGGTAAAGCGCTGAATGATAGTGTATCATGGGATT cjbiil_ai1.seq 701 AGTTGCCGATCAAAATGGTAAACCGCTGAATGATAGTGTATCATGGGATT nem316_ai1.seq AGTTGCCGATCAAAATGGTAAAGCGCTGAATGATACTCTATCATGGGATT a909_all.seq 7700 ATCATAAAACTACTTTTACAGCAACTACACATAATTACAGTTATTTAAAT Majority 7770 7780 7790 7800 ATCATAAACTACTTTTACAGCAACTACACTACAGTTATTTAAAT 2603_ail.seq 744 ATCATAAAACTACTTTTACAGCAACTACACATAATTACAGTTATTTAAAT 18rs21_ai1.seq '517 749 ATCATAAAACTACTTTTACAGCAACTACATAATTACAGTTATTTAAAT cohi_aii.seq ATCATAAAACTACTTTTACACCAACTACATAATTACAGTTATTTAAAT cjb111_ai1.seq 749 ATCATAAAACTACTTTTACAGCAACTACATAATTACAGTTATTTAAAT nem316_aii.seq 751 ATCATAAAACTACTTTTACAGCAACTACACATAATTACAGTTATTTAAAT a909_all.seq 750 TTAACAAATGATGCTAACGAAGTTAATATTCTAAAGTCAAGAATTCCAAA Majority 781Ô 7820 7830 . 7840 7850 794. TTAACAAATGATGCTAACGAAGTTAATATTCTAAAGTCAAGAATTCCAAA 2603_ai1.seq TTAACAAATGATGCTAACGAAGTTAATATTCTAAAGTCAAGAATTCCAAA 18rs21_a11.seq 567 TTAACAAATGATGCTAACGAAGTTAATATTCTAAAGTCAAGAATTCCAAA cohlail.seq 799 TTAACAAATGATGCTAACGAAGTTAATTCTAAAGTCAAGAATTCCAAA cjb111_at1.seq 799 TTAACAAATGATGCTAACGAAGTTAATTCTAAAGTCAAGAATTCCAAA nem316_a11.seq 801 TTAACAAATGATGCTAACGAAGTTAATTCTAAAGTCAAGAATTCCAAA a909_aii.seq 800 GGAAGCGGAGCATATAAATGGGGATCGCACGCTCTATCAATTTGGTGCGA Majority 7860 7870 7880 7890 7900 GGAAGCCGAGCATATAAATGGGGATCGCACGCTCTATCAATTTGGTGCGA 2603_ail.seq 844 G G A A G C G G A G C A T A T A A A T G G G G A T C G C A C G C T C T A T C A A T T T G G T G C G A 18rs21_a11.seq 617 G G A A G C G G A G C A T A T A A A T G G G G A T C G C A C G C T C T A T C A A T T T G G T G C G A cohl_ail.seq 849 GGAAGCGGAGCATATAAATGGGGATCGCACGCTCTATCAATTTGGTGCGA cjbiil_ail.seq 849 G G A A G C G G A G C A T A T A A A T G G G G A T C G C A C G C T C T A T C A A T T T G G T G C G A nem316_ai1.seq 851 GGAAGCGGAGCATATAAATGGGGATCGCACGCTCTATCAATTTGGTGCGA a909_ail.seq CATTTACTCAAAAGCTCTAATGAAAGCAAATGAAATTTTAGAGACACAA Majority 7920 7930 7940 7950 CATTTACTCAAAAAGCTCTAATGAAAGCAAATTTTAGAGACACAA 2603_ai1.seq 894 CATTTACTCAAAAGCTCTAATGAAAGCAAATGAAATTTTAGAGACACAA 18rs21_ai1.seq 667 CATTTACTCAAAAGCTCTAATGAAAGCAAATGAAATTTTAGAGACACAA cohl_ail.seq 899 CATTTACTCAAAAGCTCTAATGAAAGCAAATGAAATTTTAGAGACACAA cjbiii_aii.seq 899 CATTTACTCAAAAAGCTCTAATGAAAGCAAATGAAATTTTAGAGACACAA.nem316_ail.seq 901 CATTTACTCAAAAGCTCTAATGAAAGCAAATGAAATTTTAGAGACACAA a909_aii.seq 900 A.GT T.CTAATGCTAGAAAAAACTTATTTTTCA.CGTAA CTCATGGTGTCC.C Majority 7960 7970 7980, 7990. 8000 AGTTCTAATGCTAGAAAAAACTTATTTTTCACGTAACTGATGGTGTCCC 2603 ail seq AGTTCTAATGCTAGAAAAAACTTATTTTTCACGTAACTGATGGTCCC 18rs21 ail seq 944 717 AGTTCTAATGCTAGAAAAAATTTTTTCACGTAACTCATGCTCCCC contail.seq **949** AGTTCTAATGCTAGAAAAAATTTTTCACGTAACTCATGCTCCCCGGGGGT **B49** 951 950

TACGATGTCTTATGCCATAAATTTTAATCCTTATATATCAACATCTTACCC Wajority 8010 8020 8030 8040 8050 TACGATGTCTTATGCCATAAATTTTAATCCTTATATATCAACATCTTACC 2603_ail.seq

TACGATGTCTTATGCCATAAATTTTAATCCTTATATCAACATCTTACC 18rs21_ai1.seq 767 TACGATGTCTTATGCCATAAATTTTAATCCTTATATATCAACATCTTACC cohl_ail.seq 999 TACGATGTCTTATGCCATAAATTTTAATCCTTATATATCAACATCTTACC cjb111_ail.seq 999 TACGATGTCTTATGCCATAAATTTTAATCCTTATATCAACATCTTACC.mem316_a11,seq 301 TACGATGTCTTATGCCATAAATTTTAATCCTTATATATCAACATCTTACC a909_ail.seq 200

Alignment Report of Al-1_augmment, using J. Hern method with Weighted residue weight table. AAAACCACLTTAATTCTTTTTTAAATTACCAGATAGAAGTGGTATT Wajority Thursday, July 29, 2004 5:46 PM 8060 8070 8080 8090 8100 AAAACCAGTTTAATTCTTTTTAAATAAATACCAGATAGAAGTGGTATT 2603_ai1.seq 7817 1049 1049 1051 3050 CTCCAAGAGGATTTTATAATCAATGGTGATGATTATCAAATAGTAAAAGG Majority 8120 8130 8140 8150 CTCCAAGAGGATTTTATAATCAATGGTGATGATTATCAAATAGTAAAAGG 2603_ai1.seq 1094 · C T C C A A G A G G A T T T T A T A A T C A A T G G T G A T G A T T A T C A A A T A G T A A A A G G 18rs21_ail.seq 1867 CTCCAAGAGGATTTTATAATCAATGGTGATGATTATCAAATAGTAAAAGG cohl_all.seq 1099 CTCCAAGAGGATTTTATAATCAATGGTGATGATTATCAAATAGTAAAAGG cjb111_a11.seq mag CTCCAAGAGGATTTTATAATCAATGGTGATGATTATCAAATAGTAAAAGG nem316_aii.seq 1101 CTCCAAGAGGATTTTATAATCAATGGTGATGATTATCAAATAGTAAAAGG a909_a11.seq HOO A G, A T G G A G A G T T T T A A A C T G T T T T C G G A T A G A A A G T T C C T G T T A C T G Majority 8160 8170 8180 -8190 8200 1144 AGATGGAGAGATTTTAAACTGTTTTCGGATAGAAAGTTCCTGTTACTG 2603_ai1.seq AGATGGAGAGAGTTTTAAACTGTTTTCGGATAGAAAGTTCCTGTTACTG 18rs21_ai1.seq 917 A G: A T G G A G A G T T T T A A A C T G T T T T C G G A T A G A A A G T T C C T G T T A C T G cohl_all.seq 1149 AGATGGAGAGAGTTTTAAACTGTTTTCGGATAGAAAGTTCCTGTTACTG cjb111_ai1.seq 1149 AGATGGAGAGAGTTTTAAACTGTTTTCGGATAGAAAGTTCCTGTTACTG nem316_ail.seq 1151 AGATGGAGAGAGTTTTAAACTGTTTTCGGATAGAAAGTTCCTGTTACTG a909_aii.seq 1150 GAGGAACGACACAAGCAGCTTATCGAGTACCGCAAAATCAACTCTCTGTA Majority 8210 8220 8230 8240 8250 GAGGAACGACAAGCAAGCATATCGAGTACCGCAAAATCAACTCTCTGTA 2603_aii.seq 194 GAGGAACGACAAGCAGCTTATCGACTACCGCAAAATCAACTCTGTA 18rs21_ail.seq 967 GAGGAACGACAAGCAGCTTATCGAGTACCGCAAAATCAACTCTGTA coh1_ai1.seq 199 GAGGAACGACACAAGCAGCTTATCGAGTACCGCAAAATCAACTCTCTGTA cjbiii_ai1.seq 199 GAGGAACGACACAACCATATCGAGTACCGCAAAATCAACTCTGTA nem316_ai1.seq 201 GAGGAACGACAAGCAGCTTATCGAGTACCGCAAAATCAACTCTGTA a909_ai1.seq 200 ATGAGTAATGAGGGATATGCAATTAATAGTGGATATATTTATCTCTATTG Majority 8270 8280 8290 8300 ATGAGTAATGAGGGATATGCAATTAATAGTGGATATATTTATCTCTATTG 2603_ai1.seq 244 ATGAGTAATGAGGGATATGCAATTAATAGTGGATATATTTATCTCTATTG 18rs21_ai1.seq 017 ATGAGTAATGAGGGATATGCAATTAATAGTGGATATATTTATCTCTATTG cohl_ail.seq 249 ATGAGTAATGAGGGATATGCAATTAATAGTGGATATATTTATCTCTATTG cjb111_ai1.seq 249 ATGAGTAATGAGGGATATGCAATTAATAGTGGATATATTTATCTCTATTG nem316_ai1.seq Ż51 ATGAGTAATGAGGGATATGCAATTAATAGTGGATATATTTATCTCTATTG a909_ai1.seq 250 G A G A G A T T A C A A C T G G G T C T A T C C A T T T G A T C C T A A G A C A A G T T T Majority 8310 8320 8330 8340 8350 GAGAGATTACAACTGGGTCTATCCATTTGATCCTAAGACAAAGAAATTT 2603_ail, seq 294 GAGAGATTACAACTGGGTCTATCCATTTGATCCTAACACAAAGATTT 18rs21 ail seq 067 GAGAGATTACAACTGGGTCTATCGATTTGATGCTAAGACAAAAGTTT cobl all seq GAGAGATTACAACTGGGTCTATCGATTTGATCCTAAGACACAAGATTT cibill all seq 299 299: GAGAGATTACAACTGGGTCTATGGATTTGATCGTAAGACAAAGTTT nem316_ail.seq GAGAGATTACAACTGGGTCTATCCATTTGATCCTAAGACAAAAGTTT a909_ail.seq 301 300 CTGCAACGAAAATCAAACTCAAACATCAACAACAATATACTT 8370 8360 8380 8390 8400 CT-GCAACGAAACAAACTCAAACTCATGGTGAGCCAACAATTATACTTT 2603_ai1.seq CTGCAACGAAACAAATCAAAACTCATGGTGAGCCAACATTATACTTT 18rs21_at1.seq 117 349 . CT G C A A C G A A A C A A A T C A A A C T C A T G G T G A G C C A A C A A C A T T A T A C T T T coh1_a11 . seq 349. CTGCAACGAAACAAATCAAAACTCATGGTGAGCCAACAACATTATACTTT cjb111_ai1.seq CTGCAACGAAACAAATCAAAACTCATGGTGAGCCAAGACATTATACTTT nem316_ail.seq 351

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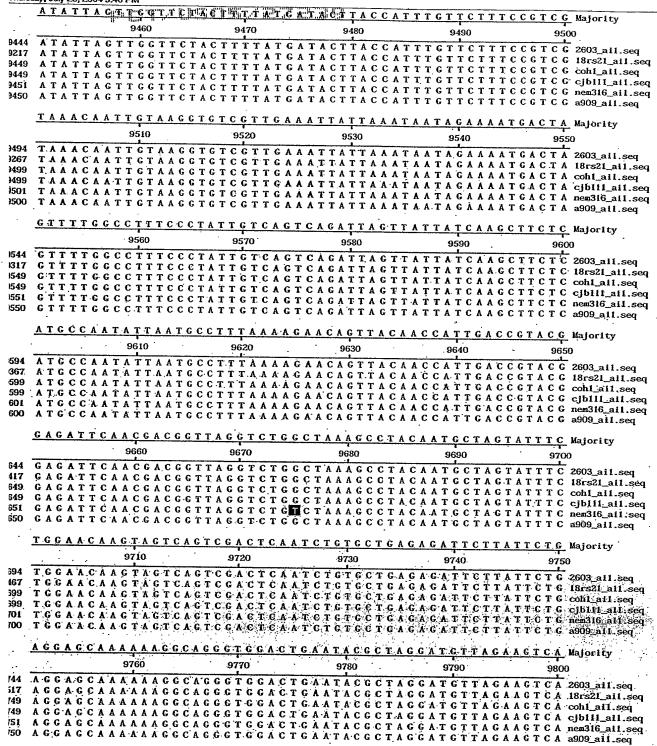
Alignment Report of Al-1 WO 2006/078318 near method with Weighted residue weight table. Thursday, July 29, 2004 5:46 PM AATCCA AATATA'ACACCA CLAA'A'AICGTTTAT CA CATTTTTACTCTTTGCCATTGC Majority 8410 8430. 8440 AATGGAAATATAAGACCTAAAGGTTATGACATTTTTACTGTTGGGATTGG 2603_ai1.seq R394 AATGGAAATATAAGACCTAAAGGTTATGACATTTTTACTGTTGGGATTGG 18rs21_ai1.seq 8167 AATGGAAATATAAGACCTAAAGGTTATGACATTTTTACTGTTGGGATTGG cohl_ai1.seq **8399** AATGGAAATATAAGACCTAAAGGTTATGACATTTTTACTGTTGGGATTGG cjbli1_ail.seq **B399** AATGGAAATATAAGACCTAAAGGTTATGACATTTTTACTGTTGGGATTGG nem316_ai1.seq 8401 8400 AATGGAAATATAAGACCTAAAGGTTATGACATTTTTACTCTTTGGGATTGG a909_ail.seq TGTAAACGGAGATCCTGGTGCAACTCCTTGAAGCTGAGAATTTATGC Majority 8460 8470 8480 849N 8500 TGTAAACGGAGATCCTGGTGCAACTCCTCTTGAAGCTGAGAATTTATGC 2603_aii.seq **B444** TGTAAACGGAGATCCTGGTGCAACTCCTCTTGAAGCTGAGAATTTATGC 18rs21_all.seq 8217 TGTAAACGGAGATCCTGGTGCAACTCCTCTTGAAGCTGAGAAATTTATGC cohl_aii.seq **B449** TGTAAACGGAGATCCTGGTGCAACTCCTCTTGAAGCTGAGAATTTATGC cjb111_ai1.seq **B449** TGTAAACGGAGATCCTGGTGCAACTCCTCTTGAAGCTGAGAATTTATGC nem316_a11.seq TGTAAACGGAGATCCTGGTGCAACTCCTTTGAAGCTGAGAATTTATGC a909_ail.seq B450 AATCAATATCAAGTAAAACAGAAATTATACTAATGTTGATGATACAAAT Majority 8520 8530 8540 8550 AATCAATATCAAGTAAAACAGAAAATTATACTAATGTTGATGATACAAAT 2603_aii.seq **B267** AATCAATATCAAGTAAAACAGAAAATTATACTAATGTTGATGATACAAAT 18rs21_a11.seq AATCAATATCAAGTAAAACAGAAAATTATACTAATGTTGATGATACAAAT cohl_ail.seq AATCAATATCAAGTAAAACAGAAAATTATACTAATGTTGATGATACAAAT cjblil_ail.seq AATCAATATCAAGTAAAACAGAAAATTATACTAATGTTGATGATACAAAT nem316_ai1.seq 3501 **8500** AATCAATATCAAGTAAAACAGAAAATTATACTAATGTTGATGATACAAAT a909_ail.seq AAAATTTATGATGAGCTAAATAATTTTAAAACAATTGTTGAGGAAAA Majority 8570 · 8580 8590 . . 8600 3544 AAAATTTATGATGAGGTAAATAATACTTTAAAACAATTGTTGAGGAAAA 2603_aii.seq AAAATTTATGATGAGCTAAATAAATACTTTAAAACAATTGTTGAGGAAAA 18rs21_ai1.seq 3317 AAAATTTATGATGAGCTAAATAAATAAATAAAAAAAAATTGTTGAGGAAAA cohl_a11.seq AAAATTTATGATGAGCTAAATACTTTAAAACAATTGTTGAGGAAAA cjb111_a11.seq AAAATTTATGATGAGCTAAATAAATACTTTAAAACAATTGTTGAGGAAAA nem316_ail.seq AAAATTTATGATGAGCTAAATAAATACTTTAAAACAATTGTTGAGGAAAA a909_a11.seq ACATTCTATTGTTGATGGAAATGTGACTGATCCTATGGGAGAGATGATTG Majority 8610 8630 8640 ACATTCTATTGTTGATGGAAATGTGACTGATCCTATGGGAGAGATGATTG 2603_ai1.seq 1594 ACATTCTATTGTTGATGGAAATGTGACTGATCCTATGGGAAGATGATTG 18rs21_ail.seq ACATTCTATTGTTGATGGAAATGTGACTGATCCTATGGGAGAGATGATTG cohl_ail.seq ACATTCTATTGTTGATGGAAATGTGACTGATCCTATGGGAGAGATGATTG cjbiil_ail.seq 1599 ACATTCTATTGTTGATGGAAATGTGACTGATCCTATGGGAAGATGATTG nem316_a11.seq 1601 ACATTCTATTGTTGATGGAAATGTGACTGATCCTATGGGAGAGATGATTG a909_ail.seq 1600 AATTCCAATTAAAAATGGTCAAAGTTTTACACATGATGATTACGTTTTC Majority 8670 8680 8690 8700 AATTCCAATTAAAAAATGCTCAAAGTTTTACACATGATGATTACGTTTTC 2603_aii.seq AATTCCAATTAAAAATCCTCAAACTTTTACACATGATGATTACCTTTTC 18rs21 al1 seq 417 649 AATTCCAATTAAAAAATGGTCAAAGTTTTACACATGATCATTACGTTTTC coht all seq 649 AATTCCAATTAAAAAATGGTCAAAGTTTTAGACATGATGATTACGTTTTG 61641Lali seq 651 AATTCCAATTAAAAAATGGTCAAAGTTTTA CACATGATGATTACGTTTTG nea316 all seq 8720 8730. 8740 8750 694 GTTGCAAATGATCCCACTCAATTAAAAATGGTGTGGCTCTTGGTGCACC 2603_a11.seq GTTGGAAATGATGGCAATTAAAAAATGGTGTGGCTCTTGGTGCACC 18 s21 all seq GTTGGAAATGATGGCAGTCAATTAAAAAATGGTGTGGCTCTTGGTGGCCCcohlail.seq 699 GTTGGAAATGATGGCAGTCAATTAAAAAATGGTGTGGCTCTTGGTGGACC cjb111_ai1.seq 699 GTTGGAAATGATGGCAATTAAAAAATGGTGTGGCTCTTGGTGGACC nen316_a11.seq 701 GTTGGAAATGATGGCAGTCAATTAAAAATGGTGTGGCTCTTGGTGGACC a909_ai1.seq 700

Alignment Report of Al-VO 2006/078318 Thursday, July 29, 2004 5:46 PM AAACAGFGATGGGCGGAATTTTAAAAAGATGTTACAGTGACTTATGATAAGAMajority 8760 8770 8780 8790 8800 8744 AAACAGTGATGGGGGAATTTTAAAAGATGTTACAGTGACTTATGATAAGA 2603_aii.seq AAACAGTGATGGGGGAATTTTAAAAGATGTTACAGTGACTTATGATAAGA 18rs21_ai1.seq 8749 AAACAGTGATGGGGGAATTTTAAAAGATGTTACAGTGACTTATGATAAGA cjbiii_aii.seq 8749 AAACAGTGATGGGGGGAATTTTAAAAGATGTTACAGTGACTTATGATAAGA nem316_ai1.seq 8751 AAACAGTGATGGGGGAATTTTAAAAGATGTTACAGTGACTTATGATAAGA a909_ail.seq 8750 CATCTCAAACCATCAAATCAATTCAACTTAGGAAGTGGACAAAA Majority 8810 8820 8830 8840 8850 CATCTCAAACCATCAAATCAATTGAACTTAGGAAGTGGACAAAAA 2603_ai1.seq 8794 CATCTCAAACCATCAAATCAATCATTTGAACTTAGGAAGTGGACAAAAA 18rs21_a11.seq 8567 CATCTCAAACCATCAAATCAATTTGAACTTAGGAAGTGGACAAAAA cohlaii.seq. 8799 CATCTCAAACCATCAAATCAATCATTTGAACTTAGGAAGTGGACAAAAA cjb111_ai1.seq 8799 CATCTCAAACCATCAAATCAATTTTTTTTAGGAAGTGGACAAAAA nem316_ai1.seq 1088 CATCTCAAACCATCAAATCAATTTTGAACTTAGGAAGTGGACAAAAA a909_ai1.seq 8800 GTAGTTCTTACCTATGATGTACGTTTAAAAGATAACTATATAAGTAACAA Majority 8860 8870 8880 8890 8900 GTAGTTCTTACCTATGATGTACGTTTAAAAGATAACTATAAAGTAACAA 2603_aii.seq **B844** GTAGTTETTACCTATGATGTACGTTTAAAAGATAACTATATAAGTAACAA 18rs21_ai1.seq GTAGTTCTTACCTATGATGTACGTTTAAAAGATAACTATAAAGTAACAA cohl_all.seq **B849** GTAGTTCTTACCTATGATGTACGTTTAAAAGATAACTATAAGTAA'CAA cjbiil ail seq GTAGTTCTTACCTATGATGTACGTTTAAAAGATAACTATATAAGTAACAA nem316_ail.seq B851 GTAGTTCTTACCTATGATGTACGTTTAAAAGATAACTATAAAGTAACAA a909_ai1.seq B850 ATTTTACAATACAAATAATCGTACAACGCTAAGTCCGAAGAGTGAAAAG Majority 8910 8920 8930 8940 8950 ATTTTACAATACAAATCGTACAACGCTAAGTCCGAAGAGTGAAAAAG 2603_ail.seq **B894** ATTTTACAATACAATAATCGTACAACGCTAAGTCCGAAGAGTGAAAAAG 18rs21_ai1.seq **B667** ATTTTACAATACAAATAATCGTACAACGCTAAGTCCGAAGAGTGAAAAAC cohla11.seq ATTTTACAATACAAATCGTACAACGCTAAGTCCGAAGAGTGAAAAAG cJb111_ai1.seq ATTTTACAATACAAATAATCGTACAACGCTAAGTCCGAAGAGTGAAAAAG nem316_ail.seq ATTTTACAATACAAATCGTACAACGCTAAGTCCGAAGAGTGAAAAAG a909_ai1.seq ACCAAATACTATTCGTGATTTCCCAAATTCCCAAAATTCGTGATGTTCGT Majority 8960 8970 8980 8990 9000 AACCAAATACTATTCGTGATTTCCCAAATTCCCAAAATTCGTGATGTTCGT 2603_ai1.seq 3944 AACCAAATACTATTCGTGATTTCCCAATTCCCAAAATTCGTGATGTTCGT 18rs21_ai1.seq 3717 AACCAAATACTATTCGTCATTTCCCAAATTCCCAAAATTCGTGATGTTCGT cohl_ail.seq 3949 AACCAAATACTATTCGTGATTTCCCAAATTCCCAAAATTCGTGATGTTCGT cjb111_a11.seq 3949 AACCAAATACTATTCGTGATTTCCCAAATTCCCAAAATTCGTGATGTTCGT nem316_ai1.seq 3951 AACCAAATACTATTCGTGATTTCCCAATTCCCAAAATTCGTGATGTTCGT a909_ai1.seq 3950 GAGTTTCCGGTACTAACCATCAGTAATCAGAAGAAATGGGTGAGGTTGA Majorlty 9010 9020 9030 9040 9050 GAGTTTCCGGTACTAACCATCAGTAATCAGAAAATGGGTCAGGTTGA 2603 ail.seq 3994 GAGTTTCCGGTACTAACCATCAGTAATCAGAAAAATCGGGTCAEGTTGA 18rs21_all seq GAGTTTCGGGTACTAACCATCAGTAATGAGAAAATGGGTGACGTTGA cohtail, seq GAGTTTCCGGCTACTAACCATCAGTAATCAGAAAATGGGTGAGGTTCA ejbill ail seq GAGTTTCCGGGTACTAACCATCAGTAATCAGAAAATCGGGTCAGGTTGA nem316 all seq DOO GAGTTTCCGGTACTACCATCACTAATCACAAAAAATGGGTGAGGTTGA ATTTATTA AAGTTAATAAACACAAACATTCACAATCCCTTTTGGGACCTA Hajority 9060 9070 9080 9090 . 9100 ATTTATTAAAGTTAATAAAGACAAACATTCAGAATCGCTTTTGGGAGCTA 2603_ail.seq 1044 ATTTATTAAAGTTAATAAAGACAAACATTCAGAATCGCTTTTGGGGAGCTA 18rs21_a11.seq **1817** ATTTATTAAAGTTAATAAAGACAAACATTCAGAAATCGCTTTTGGGGAGCTA cohl_ail.seq 1049 ATTTATTAAAAGTTAAATAAAGACAAACATTCAGAATCGCTTTTGGGAAGCTA cjb111_ai1.seq 1049 1051

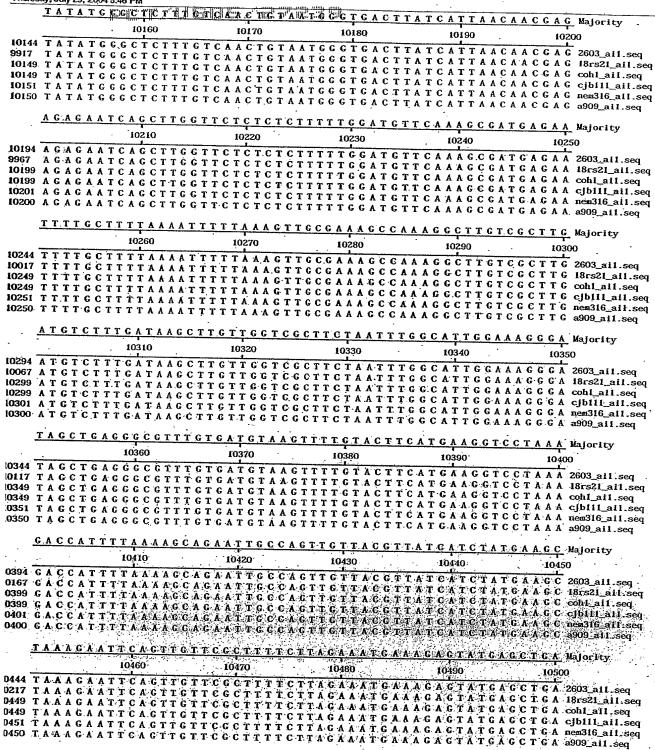
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Alignment Report of Al-1 \underline{WO} 2006/078318 method with Weighted residue weight table Thursday, July 29, 2004 5:46 PM

AGTTTC AND THE CAR AND AND AND AND AND THE TETTCEGGTATAAGCAATTTGTT Majority 9110 9120 9140 9150 AGTTTCAACTTCAGATAGAAAAGATTTTTCTGGGTATAAGCAATTTGTT 2603_ail.seq 9094 8867 AGTTTCAACTTCAGATAGAAAAAGATTTTTCTGGGTATAAGCAATTTGTT 18rs21_ai1.seq AGTTTCAACTTCAGATAGAAAAGATTTTTCTGGGTATAAGCAATTTGTT cohl_ail.seq 9099 AGTTTCAACTTCAGATAGAAAAGATTTTTCTGGGTATAAGCAATTTGTT cjb111_ai1.seq 9099 AGTTTCAACTTCAGATAGAAAAGATTTTTCTGGGTATAAGCAATTTGTT nem316_ai1.seq 9101 AGTTTCAACTTCAGATAGAAAAGATTTTTCTGGGTATAAGCAATTTGTT a909_a11.seq 9100 9160 9170 9180 9190 9200 **B144** B917 9149 **B149** 9151 9150 A.G.C.A.C.T.T.C.A.A.G.T.C.G.T.A.A.A.T.T.A.T.G.A.A.T.T.T.C.A.A.G.T.C.C.A.G.A.T.C. Majority 921**0** 9220 9230 9240 . 9250 AGCACTTCAAGATGGTAACTATAAATTATGAAATTTCAAGTCCAGATG 2603_aii.seq 1194 AGCACTTCAAGATGGTAACTATAAATTATTGAAATTTCAAGTCCAGATG 18rs21_a11.seq 1967 A G:C A C T T C A A G A T G G T A A C T A T A A A T T A T A T G A A A T T T C A A G T C C A G A T G cohi_aif.seq 1199 A G C A C T T C A A C A T G G T A A C T A T A A A T T A T A T G A A A T T T C A A G T C C A G A T G cjbii1_ai1.seq 1199 AGCACTTCAAGATGGTAACTATAAATTATATGAAATTTCAAGTCCAGATG nem316_aii.seq 1201 1200 AGCACTTCAAGATGGTAACTATAAATTATGAAATTTCAAGTCCAGATG a909_aii.seq GCTATATAGAGGTTAAAACCAAACCTGTTGTCACAATTTACAAAAT Majority 9260 9270 9280 9290 9300 244 GCTATATAGAGGTTAAAACGAAACCTGTTGTGACATTTACAAATTCAAAAT 2603_a11.seq 1017 . G C T A T A T A G A G G T T A A A A C G A A A C C T G T T G T G A C A T T T A C A A T T C A A A A T 18rs21_ail.seq GCTATATAGAGGTTAAAACCAAACCTTTTGTGACATTTACAAAAT cohl_ail.seq GCTATATAGAGGTTAAAACGAAACCTGTTGTGACATTTACAATTCÄAAAT cjbiii_aii.seq GCTATATAGAGGTTAAAACGAAACCTGTTGTGACATTTACAAATTCAAAAT nem316_at1.seq 251 GCTATATAGAGGTTAAAACGAAACCTGTTGTGAGATTTACAAATTCAAAAT a909_ail.seq 250 G G A G A A G T T A C G A A C C T G A A A G C A G A T C C A A A T G C T A A T A A A A T C A A A T Majority 9310 9320 9340 CGAGAAGTTACGAACCTGAAAGCAGATCCAAAT.GCTAATAAAAAT.CAAAT 2603_aii.seq 294 G G A G A A G T T A C G A A C C T G A A A G C A G A T C C A A A T G C T A A T A A A A T C A A A T 18rsZ1_ai1.seq 067 G G A G A A G T T A C G A A C C T G A A A G C A G A T C C A A A T G C T A A T A A A A T C A A A T cohi_ail.seq 299 G G A G A A G T T A C G A A C C T G A A A G C A G A T C C A A A T G C T A A T A A A A T C A A A T cjbiii_aii.seq 299 G G A G A A G T T A C G A A C C T G A A A G C A G A T C C A A A T G C T A A T A A A A T C A A A T nem316_ai1.seq 301 G G A G A A G T T A C C A A C C T G A A A G C A G A T C C A A A T G C T A A T A A A A T C A A A T a909_ai1.seq 300 CGGGTATCTTGAAGGAAATGGTAAACATCTTATTACCAACACTCCCAAAC Majority 9360 9370 . 9380 9390 9400 344 CGGGTATCTTGAAGGAAATGGTAAACATCTTATTACCAACACTCCCAAAC 18rs21 ail seq 117. CGGGTATCTTGAAGGAAATGGTAAACATCTTATTACCAACACTCCCAAAC 349 CGGGTATETTGAAGGAAATGGTAAACATCTTATTACCAACACTGCGAAACCJbiil all seq 349 CGGGTATCTTGAAGGAAATGGTAAACATCTTATTACCAACACTCGCAAAC nen316 all seq 351 C G G G T A T C T T G A A G G A A A T G G T A A A G A T C T T A T T A C C A X C A C T C C C A A A C a909_all.seq 350 GCCCACCAGGTGTTTTTCCTAAAACAGGGGGAATTGGTAAAATTGTCTAT Majority 9410 9420 9430 9440 9450 GCCCACCAGGTGTTTTTCCTAAAACAGGGGGAATTGGTACAATTGTCTAT 2603_ail.seq GCCCACCAGGTGTTTTCCTAAAACAGGGGGAATTGGTACAATTGTCTAT 18rs21_ail.seq 167 G C C C A C C A G C T G T T T T T C C T A A A A C A G G G G G A A T T G G T A C A A T T G T C T A T cohi_ail.seq 199 GCCCACCAGGTGTTTTTCCTAAAACAGGGGGAATTGGTACAATTGTCTAT cjb111_ail.seq 199 GCCCACCAGGTGTTTTCCTAAAACAGGGGGAATTGGTACAATTGTCTAT nem316_ail.seq 101 GCCCACCAGGTGTTTTCCTAAAACAGGGGGAATTGGTAAAATTGTCTAT a909_a11.seq 100



9810 9820 9830 9840 GAGAGCAGGTTGACCATGTGATCCAAAAATCAATCAGGATTTACCA 2603_ail.seq 794 1567 GAGAGCAGGTTGACCATGTGATCCAAAAATCAATCAGGATTTACCA cohl_ail.seq 1799 1799 ROI CAGAGCAGGTTGACCATGTGATCAATCAAAAATCAATCAGGATTTACCA a909_a11.seq 1800 ATCTACCCTGGTTCAGAAGAGGACAATCTGCAACGGGGAGTTGGTCATCT Majority 9860 9870 9880 9890 9900 ATCTACCCTGGTTCAGAAGAGGACAATCTGCAACGGGGAGTTGGTCATCT 2603_ail.seq 1844 ATCTACGCTGGTTCAGAAGAGGACAATCTGCAACGGGGAGTTGGTCATCT 18rs21_ai1.seq 1617 ATCTACCCTGGTTCAGAAGACGACAATCTGCAACGGGGAGTTGGTCATCT cohl_all.seq 1849 ATCTACGCTGGTTCAGAAGAGGACAATCTGCAACGGGGAGTTGGTCATCT cjb111_ai1.seq IR49 ATCTACGCTGGTCACAGAGAGACACGACAACCGGGGAGTTGGTCATCT nem316_ail.seq 1851 ATCTACGCTGGTTCAGAAGAGGACAATCTGCAACGGGGAGTTGGTCATCT a909_ail.seq 1850 A G-A A G G G A T A A G T T T G C C G A T T G G A G G G G C T T C T A C A C A T G C G G T C T T G A Majority 9910 9920 9930 9940 9950 AGAAGGGATAAGTTTGCCGATTGGAGGGGCTTCTACACATGCGGTCTTGA 2603_ai1.seq 894 AGAAGGGATAAGTTTGCCGATTGGAGGGGCTTCTACACATGCGGTCTTGA 18rs21_ai1.seq AGAAGGGATAAGTTTGCCGATTGGAGGGGCTTCTACACATGCGGTCTTGA cohl_ai1.seq A G A A G G G A T A A G T T T G C C G A T T G G A G G G G C T T C T A C A C A T G C G G T C T T G A cjb111_a11.seq AGAAGGGATAAGTTTGCCGATTGGAGGGGCTTCTACACATGCGGTCTTGA nem316_ail.seq 901 AGAAGGGATAAGTTTGCCGATTGGACGGGCTTCTACACATGCGGTCTTGA a909_ai1.seq GCGGTCAAAGAGGTATGCCAGCTGCTCGCTTGTTTGCGGATTTGGATAAG Majority 9960 9970 9980 9990 10000 GCGGTCAAAGAGGTATGCCAGCTGCTCGGTTGTTTGCGGATTTGGATAAG 2603_ai1.seq GCGGTCAAAGAGGTATGCCAGCTGCTCGGTTGTTTGCGGATTTGGATAAG 18rs21_ail.seq GCGGTCAAAGAGGTATCCCAGCTGCTCGGTTGTTTGCGGATTTGGATAAG coh1_ai1.seq GCGGTCAAAGAGGTATGTCAGCTGCTCGGTTGTTTGCGGATTTGGATAAG cjbiil_aii.seq GCGGTCAAAGAGGTATGTCAGCTGGTTGTTTGCGGATTAGGATAAG a909_ai1.seq ATGAAAAAGGTGATTATTTTTATGTTACCAATCTGAAAGAACCTTGGC Majority 10010 10020 10030 10040 10050 ATGAAAAAGGTGATTATTTTTTATGTTACCAATCTGAAAGAACCTTGGC 2603_ai1.seq 994 ATGAAAAAGGTGATTATTTTTATGTTACCAATCTGAAAGAACCTTGGC 18rs21_a11.seq 767 999 ATGAAAAAGGTGATTATTTTTATGTTACCAATCTGAAAGAACCTTGGC cjb111_ai1.seq 0001 ATCAAAAAGGTGATTATTTTTATGTTACCAATCTGAAAGAACCTTGGC nem316_aii.seq 0000 ATGAAAAAGGTGATT.ATTTTTTTCCCAATCTGAAAGAACCTTGGC a909_ail.seq TTATCAAGTGGATCGTATCATGGTGATTGAACCTAGCCAATTGGATGCCG Majority 10060 10070 10080 10090 10100 DO44 TTATCAAGTGGATCGTATCATGGTGATTGAACCTAGCCAATTGGATGCCG 2603_a11.seq BIT TTATCAACTGGATCGTATCATGGTGATTGAACCTAGCCAATTGGATGGCATGGCA DO49 TTATCAAGTGGATGGTATCATGGTGATTGAACCTAGCGAATTGGATGCCG DO49 TTATCAAGTGGATCGTATCATGGTGATTGAACCTAGCCAATTGGATGCCCGCIBHIL GAIL Seq DOSI TTATCAAGTGGATCGTATCATGGTGATTGAACCTAGCCAATTGGATGCCCATGGCATGGGATGGG DOSO TTATCAAGTGGATGGTATCATGGTGATTGAACCTAGCCAATTGGATGCCG a909 all seq T G A G C A T T G A A G A G C A T A A A G A T T A T G T T A G C C T T C T G A C G T G T A C A C C T Hajority 10110 10120 10130 10140 10150 DO94 T G A G C A T T G A A G A G G A T A A A G A T T A T G T T A C C C T T C T G A C C T G T A C A C C T 2603_at1.seq BG7 TGAGCATTGAAGAGGATAAAGATTATGTTACCCTTCTGACCTGTACACCT 18rs21_a11.seq DO99 TGAGCATTGAAGAGGATAAAGATTATGTTACCCTTCTGACCTGTACACCT coni_aii.seq. DO99 TGAGCATTGAAGAGGATAAAGATTATGTTACCCTTCTGACCTGTACACCT cjb111_a11.seq DIOI T.G.A.G.C.A.T.T.G.A.A.G.A.T.T.A.T.G.T.T.A.C.C.C.T.T.C.T.G.A.C.C.T.G.T.A.C.A.C.C.T. nem316_ai1.seq DIOO: T G A G C A T T G A A G A G G A T A A A G A T T A T G T T A C C C T T C T G A C C T G T A C A C C T a909_ail.seq



Alignment Report of Al-1_alignment, using J. Hein method with Weighted residue weight table. Thursday, July 29, 2004 5:46 RM Thursday, July 29, 2004 5:46 PM 11:00 TAAAGGTGGTTÄTÄÄ TACCCCACCTCATCTCAGAAAACTTTTATACCTCA Majority 10510 10520 10530 10540 10494 TAAAGGTCGTTATAATAGCGGAGCTCATCTGAGAAACTTTTATACCTCA 2603_ail.seq 10267 TAAAGGTCGTTATAATAGCGGAGCTCATCTGAGAAACTTTTATACCTCA 18rs21_ail.seq 10499 TAAAGGTCGTTATAATAGCGGAGCTCATCTGAGAAACTTTTATACCTCA cohi_aii.seq 10499 TAAAGGTCGTTATAATAGCGGAGCTCATCTGAGAAAACTTTTATACCTCA cjb111_ai1.seq 10501 TAAAGGTCGTTATAATAGCGGAGCTCATCTGAGAAAACTTTTATACCTCA nem316_ail.seq 10500 TAAAGGTCGTTATAATAGCGGAGCTCATCTGAGAAAACTTTTATACCTCA a909_a11.seq AGTCAGTCTAGCTTTGATATCATGAAGCCATTAGGAGTTATTCCTTATC Majority 10560 10570 10580 10590 10600 10544 AAGTCAGTCTAGCTTTGATATCATGAAGCCATTAGGAGTTATTCCTTATC 2603_ai1.seq 10317 AAGTCAGTCTAGCTTTGATATCATGAAGCCATTAGGAGTTATTCCTTATC 18rs21_ai1.seq 10549 AAGTCAGTCTAGCTTTGATATCATGAAGCCATTAGGAGTTATTCCTTATC cohlail.seq 10549 AAGTCAGTCTAGCTTTGATATCATGAAGCCATTAGGAGTTATTCCTTATC cjb111_ai1.seq 10551 AAGTCAGTCTAGCTTTGATATCATGAAGCCATTAGGAGTTATTCCTTATC nem316_ail.seq 10550 AAGTCAGTCTAGCTTTGATATCATGAAGCCATTAGGAGTTATTCCTTATC a909_ail.seq TTTTAGTGGCGCGCGATCCATATAGTGATAGATCGAGATATTTAGATCCA Majority 10620 10630 10640 10594 TTTTAGTGGCGCGCGATCCATATAGTGATAGATCGAGATATTTAGATCCA 2603_ai1.seq . 10367 TTTTAGTGGCGCGCGATCCATATAGTGATAGATCGAGATATTTAGATCCA 18rs21_all.seq 10599 TTTTAGTGGCGCGCGATCCATATAGTGATAGATCGAGATATTTAGATCCA cohlail.seq TTTTAGTGGCGCGCGATCCATATAGTGATAGATCGAGATATTTAGATCCA cjb111_ai1.seq 10599 T.T.T.T.A.G.T.G.G.C.G.C.G.G.A.T.C.C.A.T.A.T.A.G.T.G.A.T.A.G.A.T.C.G.A.G.A.T.A.T.T.A.G.A.T.C.G.A. nem316_ai1.seq 10601 TTTTAGTGGCGCGCGATCCATATAGTGATAGATCGAGATATTTAGATCCA a909_ail.seq 10600 AAAGTTCTATCATCCTCTTTTGGCGCCCTTTTTTCCAGCAGATAATATTAA Majority 10660 10670 10680 10690 10700 10644 AAAGTTCTATCATCCTCTTTTGGCGCCCTTTTTCCAGCAGATAATATTAA 2603_ai1.seq 10417 AAAGTTCTATCATCCTCTTTTGGGGGCCTTTTTTCCAGCAGATAATATTAA 18rs21_ai1.seq 10649 AAAGTTCTATCATCCTCTTTTCGCCCCTTTTTTCCAGCAGATAATATTAA cohi_aii.seq 10649 A.A.A.G.TTCTATCATCCTCTTTTGGCCCCTTTTTTCCAGCAGATAATATTAA cjbiil_ail.seq 10651 AAAGTTCTATCATCCTCTTTTGGCGCCCTTTTTTCCAGCAGATAATATTAA nem316_ail.seq 10650 AAAGTTCTATCATCCTCTTTTGGCGCGCTTTTTCCCAGCAGATAATATTAA a909_a11.seq GGTAGCTTGGTCTAACAACTCCAGCAGTTTATTTACACCACCTATTAATG Majority 10720 10730 10740 .0694 G G T A G C T T G G T C T A A C A A C T C C A G C A C T T T A T T T A C A C C A C C T A T T A A T G 2603_ail.seq O467 GGTAGCTTGGTCTAACAACTCCAGCACTTTATTTACACCACCTATTAATC 18rs21_ai1.seq 0699 GGTAGCTTGGTCTAACAACTCCAGCACTTTATTTACACCACCTATTAATG cjb111_ail.seq 0699 0701 GGTAGCTTGGTCTAACAACTCCAGCACTTTATTTACACCACCTATTAATG nem316_ail.seq 0700 G G T A G C T T G G T C T A A C A A C T C C A G C A C T T T A T T T A C A C C A C C T A T T A A T G a909_ail.seq CAAACTACACCACTCAGATTCAAGCTATTGGGAAACGATTAAGTCACAA Majority 10760 10770 10780 10790 0744 CAAACTACACCACTCAGATTCAAGCTATTGGGGACAACGATTAAGTCACAA 2603_all.seq 0749 CAAACTACACCACTCAGATTCAAGCTATTGGGAAACGATTAAGTCACAA cohl all seq 0749 CAAACTACACCACTCACATTCAACCTATTCCGCACAACCATTAACTCACAACIbiil ail seq O751 CAAACTACACCACTCACATTCAACCTATTCGGGACAAGCATTAACTCACAA nem316_aii.seq 0750 CAAACTACACCAGTCAGATTCAACCTATTCGCAACAACCATTAAGICACAA a909 all seq ATTCCCCCAATCCAATTTCACCCTTACCCAAAAAAAGCCACAAGTTCAC 10810 10820 10830 10840 10850 0794 ATT CCGGAATCGATTTTGACGGTTACGGATAAAAAGAGCAGGAAGTTCAG 2603_all.seq 0567 ATTCCGGAATCGATTTTGACGGTTACGGATAAAAGAGCAGGAAGTTCAG 18rs21_a11.seq 0799 ATTCCGGAATCGATTTTGACGGTTACGGATAAAAAGAGCAGGAAGTTCAG cohl_all.seq 0799 ATTCCGGAATCGATTTTGACGGTTACGGATAAAAGAGCAGGAAGTTCAC cjbili_ail.seq 0801 ATTCCGGAATCGATTTTGACGATTAACGGATAAAAAGAGCAGGAAGTTCAG nem316_ai1.seq

0800 ATTCCCGAATCGATTTTGACGGTTACGGATAAAAGAGCAGGAAGTTCAG a909_ail.seq

Alignment Report of Al- WQ~2006/078318 method with Weighted residue weight table Thursday, July 29, 2004 5:46 PM CATTAA CAMA GA AT TO A SOLO ATA GOT A ANA GA A G C CTTAGTAGGTGC GACCTTCA Majority 10860 10870 10880 10890 10900 10844 CATTAACAAGATTGACGAAGCTAAAGAAGCTTAGTAGCTGCGACCTTCA 2603_aii.seq 10617 CATTAACAAGATTGACGAAGCTAAAGAAGGCTTAGTAGGTGCGACCTTCA 18rs21_ai1.seq 10849 CATTAACAAGATTGACGAAGCTAAAGAAGGCTTAGTAGGTGCGACCTTCA cohl_ail.seq 10849 CATTAACAAGATTGACGAAGCTAAAGAAGGCTTAGTAGGTGCGACCTTCA cjb111_ai1.seq 10851 CATTAACAAGATTGACGAAGCTAAAGAAGGCTTAGTAGGTGCGACCTTCA nem316_ai1.seq 10850 CATTAACAAGATTGACGA'AGCTAAAGAAGGCTTAGTAGGTCCGACCTTCA a909_ail.seq C C T T G T C T A A A C G C A C A C A G T A G C G G C A G A T C A T C A A G T A C A A G G A G A T Majority 10910 10920 10930 10940 10950 10894 C CTT GT CTAAA C G CACAA CAGTAG C G G C A GAT CAT CAA G TACAA G G A G A T 2603_a11.seq 10667 C C T T G T C T A A A C G C A C A A C A G T A G C G G C A G A T C A T C A A G T A C A A G G A G A T 18rs21_ai1.seq 10899 C C T T G T C T A A A C G C A C A A C A G T A G C G G C A G A T C A T C A A G T A C A A G G A G À T 10899 CCTTGTCTAAACGCACAACAGTAGCGGCAGATCATCAAGTACAAGGAGAT cjb111_a11.seq 10901 CCTTGTCTAAACGCACAACAGTAGCGGCAGATCATCAAGTACAAGGAGAT nem316_ai1.seq 10900 C C T T G T C T A A A C G C A C A A C A G T A G C G G C A G A T C A T C A A G T A C A A G G A G A T a909_ail.seq. T T C A T T C C T G T C A G C A A A G A G A C G A C A G T C G G T C G G A C A A C C C T T A C C T T Majority 10960 10970 10980 10990 11000 10944 TTCATTCCTGTCAGCAAAGAGACGACAGTCGGTCGGACAACCCTTACCTT 2603_aii.seq 10717 TTCATTCCTGTCAGCAAAGAGACGACGACGGTCGGACAACCCTTACCTT 18rs21_ai1.seq 10949 TT:CATTCCTGTCAGCAAAGACACGACAGTCGGTCGGACAACCCTTACCTT cohl_ail.seq 10949 TTCATTCCTGTCAGCAAAGAGACGACAGTCGGTCGGACAACTCTTACCTT cjb111_a1f.seq. 10951 TTCATTCCTGTCAGCAAAGAGAGACGACAGTCGGTCGGACAACCCTTACCTT nem316_ai1.seq .0950 TTCATTCCTGTCAGCAAAGAGACGACAGTCGGTCGGACAACTCTTACCTT a909_ai1.seq T G A C A A C C T T A A A C C T G G A T T T T A T G A C C T T A A A G A A C G A A A G C G C C G A Majority . 11020 11030 11040 11050 0994 T G A C A A C C T T A A A C C T G G A T T T T A T G A C C T T A A A G A A A C G A A A G C G C C G A . 2603_ail_seq O767 T. G A C A A C C T T A A A C C T G G A T T T T A T G A C C T T A A A G A A A C G A A A G C G C C G A 18rs21_a11.seq 0999 T G A C A A C C T T A A A C C T G G A T T T T A T G A C C T T A A A G A A A C G A A A G C G C C G A cohi_all.seq D999 TGACAACCTTAAACCTGGATTTTATGACCTTAAAGAAACGAAAGCGCCGA cjbli1_ai1.seq 1001 T G A C A A C C T T A A A C C T G G A T T T T A T G A C C T T A A A G A A A C G A A G C G C C G A nem316_ail.seq 1000 T G A C A A C C T T A A A C C T G G A T T T T A T G A C C T T A A A G A A A G C G C C G A a909_aii.seq ATGCTTACGTACTTGATCCTAAGACTTATGTTGTGGTCGTTCAAAATTCA Majority 11060 11070 11080 11090 11100 1044 ATGCTTACGTACTTGATCCTAAGACTTATGTTGTGGTCGTTCAAAATTCA 2603_ai1.seq D817 ATGCTTACGTACTTGATCCTAAGACTTATGTTGTGGTCGTTCAAAATTCA 18rs21_ai1.seq 1049 ATGCTTACGTACTTGATCCTAAGACTTATGTTGTGGTCGTTCAAAATTCA cohi_ai1.seq 1049 ATGCTTACGTACTTGATCCTAAGACTTATGTTGTGGTCGTTCAAAATTCA cjbiii_aii.seq 1051 ATGCTTACGTACTTGATCCTAAGACTTATGTTGTGGTCGTTCAAAATTCA nem316_a11.seq 1050 ATGCTTACGTACTTGATCCTAAGACTTATGTTGTGGTCGTTCAAAATTCA a909_ai1.seq G C A A A A A C G A C A A T T C T C G A T C A A C C T A A C T T C A A A G A G G C T G A T T A C C C Majority 11110 11120 11130 11140 11150 1094 G G A A A A A C G A C A A T T G T G G A T G A A G C T A A C T T C A A A G A G C C T G A T T A C C C 2603_a11.seq B67 C C A A A A A C C A C A A T T C T C C A T C A A C C T A A C T T C A A A C G C T G A T T A C C C 18rs21_a11, seq [099 G G A A A A C C A C A A T T C T C G A T C A A C C T T C A A A C A C C T G A T T A C C C cohi_ai1.seq 1099 G G A A A A A C G A C A A T T G T G G A T G A A G C T A A C T T C A A A G A G G C T G A T T A C C C CIDILL all seq ITOF G GAAAAA G GACAATT GT G GAT GAAG CTAA CTT CAAAG AG G CT GATTA C G C nee316 att seq 100 C G A A A A C C A C A A T T C T C G A T C A A C C T T C A A A G A G C C T G A T T A C C C a 3009 at 1. seq 11160 11170 11180 11190 11200 144. A AT G G C T G A T A A T A C C A G C C A T C T G G A G T G C G T A G C G T T G C T A C A A C G A A 2603 all seq 1917 A AT G G C T G A T A A T A C C A G C C A T C T G G A G T G C G T A G C G T T G C T A C A A C G A A 18rs21_ail.seq 149 A ATGGCTGATAATACCAGCCATGTGCAGTGCGTAGCGTTGCTACAACGAA cohlail.seq 149 AATGGCTGATAATACCAGCGATGTGGAGTGCGTAGCCTTGCTACAACGAA cjbiil_ai1.seq 151 AATGGCTGATAATACCAGCCATGTGGAGTGCGTAGCGTTGCTACAACGAA nem316.ail.seq

Thursday, July 29, 2004 5:46 PM	
GCAAAGGGTA WAAATEGTTATTTAACGACTTTTTCAAGCATTTTGTCT Major	***
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11194 G C A A A G G G T A A A A A T C C T T T A T T T T A A G C A C T T T T T C A A G C A T T T T G T C T 2603_E	il.seq
11199 G C A A A G G G T A A A A A T C C T T T A T T T T T A A G C A C T T T T T C A A G C A T T T T G T C T 18rs21 11199 G C A A A G G G T A A A A A T C C T T T A T T T T T A A G C A C T T T T T C A A G C A T T T T G T C T cjb111	il.seq
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11249 TTATTGAAAAGAGTGATTTTAACATAAAAAAGGTATTAAAAAACATATTG cohl_a 11251 TTATTGAAAAGAGTGATTTTAACATAAAAAAGGTATTTAAAAAACATATTG ciblii	_ail.seq
11250 TTATTGAAAAGAGTGATTTTAACATAAAAAGGTATTAAAAAACATATTG nem316	_ail.seq
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11294 A C G T G A C C G T T T G T T T T G A A G T G G C T T G C G T A G A C A A A A A A A A A A C G 2603_a	il.sea
11299 A C G T G A C C G T T T G T T T T G A A G T G G C T T G C G T A G A C A A A A A A A A T A G A T A C G cohi_a 11301 A C G T G A C C G T T T G T T T T G A A G T G G C T T G C G T A G A C A A A A A A A A T A G A T A C G nem316	_ail.seq
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11349. T.C.A.G.A.T.A.A.A.T.T.T.C.T.G.G.C.A.T.T.A.C.G.A.G.A.A.C.A.T.T.T.T.A.G.A.G.T.G.T.T.C.T.C.T.T.T.T.Cohl_a	il.seq
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11351 T C A G A T A A A T T T C T G G C A T T A C G A G A A C A T T T T T A G A G T G T T C T C T T T T T c c c c c a c a a c a T T T T	all.seq all.seq ll.seq
11351 T C A G A T A A A T T T C T G G C A T T A C G A G A A C A T T T T T A G A G T G T T C T C T T T T T c c c c c a c a a c a T T T T	all.seq all.seq ll.seq
11351 T C A G A T A A A T T T C T G G C A T T A C G A G A A C A T T T T T A G A G T G T T C T C T T T T T cibili cisso T C A G A T A A A T T T C T G G C A T T A C G A G A A C A T T T T T A G A G T G T C T C T T T T T a goog a company of the compa	all.seq all.seq ll.seq
1351 T C A G A T A A A T T T C T G G C A T T A C G A G A A C A T T T T T A G A G T G T T C T C T T T T T cjb111 1350 T C A G A T A A A T T T C T G G C A T T A C G A G A A C A T T T T T A G A G T G T C T C T T T T T nem316 1350 T C A G A T A A A T T T C T G G C A T T A C G A G A A C A T T T T T A G A G T G T T C T C T T T T T a909_a TT A G T T T A C G G A G G A A A A A T A T A T A T G G A A A A	_ail.seq _ail.seq II.seq
1351 T C A G A T A A A T T T C T G G C A T T A C G A G A A C A T T T T T A G A G T G T T C T C T T T T T cjb111 1350 T C A G A T A A A T T T C T G G C A T T A C G A G A A C A T T T T T A G A G T G T T C T C T T T T T nem316 1350 T C A G A T A A A T T T C T G G C A T T A C G A G A A C A T T T T T T A G A G T G T T C T C T T T T T a909_a T T A G T T T A C G G A G G A A A A A T A T A T A T G G A A A A	_ail.seq _ail.seq ll.seq
11351 T C A G A T A A A T T T C T G G C A T T A C G A G A A C A T T T T T A G A G T G T T C T C T T T T T c c c c c c c c c c	ail.seq ail.seq II.seq
1351 T C A G A T A A A T T T C T G G C A T T A C G A G A A C A T T T T T A G A G T G T T C T C T T T T T rejbiii 1350 T C A G A T A A A T T T C T G G C A T T A C G A G A A C A T T T T T A G A G T G T T C T C T T T T T nea316. 1350 T C A G A T A A A T T T C T G G C A T T A C G A G A A C A T T T T T A G A G T G T T C T C T T T T T a909_a T T A G T T T A C G G A G G A A A A A T A T A T A T G G A A A A	ail.seq ail.seq II.seq y il.seq ail.seq
1351 T C A G A T A A A T T T C T G G C A T T A C G A G A A C A T T T T T A G A G T G T T C T C T T T T T cjb111 1350 T C A G A T A A A T T T C T G G C A T T A C G A G A A C A T T T T T A G A G T G T C T C T T T T T nem316 1350 T C A G A T A A A T T T C T G G C A T T A C G A G A A C A T T T T T A G A G T G T T C T C T T T T T a909_a T T A G T T T A C G G A G G A A A A A T A T A T A T G G A A A A	ail.seq ail.seq il.seq il.seq ail.seq ail.seq ail.seq ail.seq ail.seq
1351 T C A G A T A A A T T T C T G G C A T T A C G A G A A C A T T T T T A G A G T G T T C T C T T T T T cjb111 1350 T C A G A T A A A T T T C T G G C A T T A C G A G A A C A T T T T T A G A G T G T C T C T T T T T nem316 1350 T C A G A T A A A T T T C T G G C A T T A C G A G A A C A T T T T T A G A G T G T T C T C T T T T T a909_a T T A G T T T A C G G A G G A A A A A T A T A T A T G G A A A A	ail.seq ail.seq il.seq il.seq ail.seq ail.seq ail.seq ail.seq ail.seq
1351 T C A G A T A A A T T T C T G G C A T T A C G A G A A C A T T T T T A G A G T G T T C T C T T T T T cjb111 1350 T C A G A T A A A T T T C T G G C A T T A C G A G A A C A T T T T T A G A G T G T T C T C T T T T T nem316. 1350 T C A G A T A A A T T T C T G G C A T T A C G A G A A C A T T T T T T A G A G T G T T C T C T T T T T a909_a T T A G T T T A C G G A G G A A A A A T A T A T A T G G A A A A	ail.seq ail.seq il.seq il.seq ail.seq ail.seq ail.seq ail.seq ail.seq
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1351 T C A G A T A A A T T T C T G G C A T T A C G A G A A C A T T T T T A G A G T G T T C T C T T T T T c c c c c c c c c c	ail.seq ail.seq II.seq il.seq ail.seq ail.seq ail.seq ail.seq ail.seq
1351 T C A G A T A A A T T T C T G G C A T T A C G A G A A C A T T T T T A G A G T G T T C T C T T T T T cjb111 1350 T C A G A T A A A T T T C T G G C A T T A C G A G A A C A T T T T T A G A G T G T T C T C T T T T T nem316 1350 T C A G A T A A A T T T C T G G C A T T A C G A G A A C A T T T T T T A G A G T G T T C T C T T T T T a 909_a T T A G T T T A C G G A G G A A A A A T A T A T A T G G A A A A	ail.seq ail.seq il.seq il.seq ail.seq ail.seq ail.seq ail.seq
1351 T C A G A T A A A T T T C T G G C A T T A C G A G A A C A T T T T T A G A G T G T T C T C T T T T T replit 1 1350 T C A G A T A A A T T T C T G G C A T T A C G A G A A C A T T T T T A G A G T G T T C T C T T T T T near 16 1350 T C A G A T A A A T T T C T G G C A T T A C G A G A A C A T T T T T T A G A G T G T T C T C T T T T T a 909_a a	ail.seq ail.seq il.seq il.seq ail.seq ail.seq ail.seq ail.seq
1351 T C A G A T A A A T T T C T G G C A T T A C G A G A A C A T T T T T A G A G T G T T C T C T T T T T replit 1350 T C A G A T A A A T T T C T G G C A T T A C G A G A A C A T T T T T A G A G T G T T C T C T T T T T nem316. T T A G T T A C G G A G G A A A A A T A T A T A T G G A A A A	ail.seq ail.seq il.seq ail.seq ail.seq ail.seq ail.seq ail.seq ail.seq i.seq
1351 T C A G A T A A A T T T C T G G C A T T A C G A G A A C A T T T T T A G A G T G T T C T C T T T T T c c c c c c c c c c	ail.seq ail.seq il.seq il.seq ail.seq ail.seq ail.seq ail.seq ail.seq il.seq ail.seq
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11351 T C A G A T A A A T T T C T G G C A T T A C G A G A A C A T T T T A G A G T G T T C T C T T T T T G G G I G T A C A T T T T T A G A G T G T C T C T T T T T T nem316, 11350 T C A G A T A A A T T T C T G G C A T T A C G A G A A C A T T T T T A G A G T G T T C T C T T T T T nem316, 11350 T C A G A T A A A T T T C T G G C A T T A C G A G A A C A T T T T T T A G A G T G T T C T C T T T T T a 709 a T T A G T T T A C G G A G G A A A A A T A T A T A T A T A	ail.seq ail.seq il.seq ail.seq ail.seq ail.seq ail.seq ail.seq ail.seq ail.seq ail.seq ail.seq
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11351 T C A G A T A A A T T T C T G G C A T T A C G A G A A C A T T T T T T A G A G T G T T C T C T T T T T 1 11351 T C A G A T A A A T T T C T G G C A T T A C G A G A A C A T T T T T T A G A G T G T T C T C T T T T T 1 1 11350 T C A G A T A A A T T T C T G G C A T T A C G A G A A C A T T T T T T T A G A G T G T T C T C T T T T T 1 1 11300 T 1 1410 T 1420 T 1430 T 1440 T 1450 1.1394 T T A G T T T A C G G A G C A A A A A T A T A T A T A T G G A A A A	ail.seq ail.seq il.seq ail.seq
1351 T C A G A T A A A T T T C T G G C A T T A C G A G A A C A T T T T T T A G A G T G T T C T C T T T T T 1 1351 1350 T C A G A T A A A T T T C T G G C A T T A C G A G A A C A T T T T T T A G A G T G T T C T C T T T T T 1 1360 136 1350 T C A G A T A A A T T T C T G G C A T T A C G A G A A C A T T T T T T T T A G A G T G T T C T C T T T T T 1 1360 136 1350 T C A G A T A A A T T T C T G G C A T A C A C A A A A C A G G A T T C A C G A G T T C T T T T T 1 1450 11420 11430 11440 11450 11550	ail.seq ail.seq il.seq ail.seq ail.seq ail.seq il.seq ail.seq ail.seq il.seq ail.seq il.seq il.seq il.seq il.seq il.seq il.seq ail.seq il.seq il.seq ail.seq
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1351 T C A G A T A A A T T T C T C G C A T T A C G A G A C A T T T T T A G A G T G T T C T C T T T T T T 1 16 11 11 11 11	ail.seq ail.seq il.seq ail.seq ail.seq il.seq ail.seq ail.seq il.seq il.seq ail.seq il.seq ail.seq ail.seq ail.seq ail.seq ail.seq ail.seq ail.seq ail.seq
1351 T C A G A T A A A T T T C T C G C A T T A C G A G A A C A T T T T T A G A G T G T T C T T T T T T T G G L A T A A A T T T C T C G C C A T T A C G A G A A C A T T T T T T A G A G T G T T C T C T T T T T A G A G T G T T C T C T T T T T A G A G T G T T C T C T T T T T A G A G T G T T C T C T T T T T A G A G T G T T C T C T T T T T A G A G T G T T C T C T T T T T A G A G T G T T C T C T T T T T A G A G T G T T C T C T T T T T A G A G T G T T C T C T T T T T A G A G T G T T C A C G A C T T C T T T T T A G A G T T C A C G A C T T C A C C A A A C C	ail.seq ail.seq il.seq ail.seq ail.seq il.seq ail.seq ail.seq il.seq il.seq ail.seq

age 34

Thurs	lay, July 29, 2004 5	:46 PM	o leuloù with vvergnted res	idue weight table.		1 0 17 0 5 2 0 0 0 7
	GGGGAAC	CCCCACA	ATIGAT C'GA A'A	GG ACTAGAAAG	TGTCCGTAATGA	T Valority
		11560	11570	11580		•
11544	GGGGAAC	CGCCCAGA	ATGATCCAAA	CCCACTACAAA		600
11551	GGGGAAC	CGCCCAGA	ATGATCCAAAA	CCACTACAAAG	TGTCCGTAATGA	T cjbill_ail.seq
11550	GGGGAAC	CGCCCAGA	ATGATCCAAA (GGCACTAGAAAG	T G T C C G T A A T G A 1 T G T C C G T A A T G A 1	T nem316_ail.seq
	ICGAIII	CEGECEGTE	ATGATGTCAT	GGGTTATGCTT	ATAGCAAATGTAC	Majority
		11610	11620	11630	11640	, 650
11594	TCGATTT	CGGGGGGT	GATGATGTCA1	GGGTTATGCTT	ATAGCAAATGTAC	C 2603 all seg
11599	TCGATTT	CGGGCGGT	CATGATGICAT	CCCTTATCCTT	ATAGCAAATGTAC	Cohl_ail.seq
11600	ICGATTT	CCCCCCCTC	GATGATGTCAT	G G G T T A T G C T.T A	A T A G C A A A T G T A C A T A G C A A A T G T A C	a909_all.seq
•					A C T C A A A G G T T G	
		11660	11670		4	
1644	TTCCCCA			11680	11690 117	700
					A A C T C A A A G G T T G	
					A A C T C A A A G G T T G	
	AAATGGT	GAGAAGATT	ACCATTACCA	GTTCAATGGGAA	ATGGTCAGGATT	Majority
		11710	11720	11730	11740 117	•
1694	AAATGGT	GAGAAGATT	ACCATTACCA	GTTCAATGGGAA	1 2 2 2 2 2 2 2 2	-
1699	AAATGGT	GAGAAGATT	ACCATTACCA	CTTCAATGGGAA	ATGGTCAGGATT	cohl_all.seq
1700	AAATGGT	GAGAAGATT	ACCATTACCA	GTTCAATGGGAA	A T G G T C A G G A T T A T G G T C A G G A T T	a909_ail.seq
					ACAGTTCCAAAA	
		11760	11770	11780		*
1744	GGGTTGG	•				
					A C A G T T C C A A A A A C A G T T C C A A A A	
					A C A G T T C C A A A A A C A G T T C C A A A A	
	G A A.G G T A C	TATTCTCT	CTTTTTAGGA-	AAGTAGTTATGG	TTCGTATATAGG	Majority
		11810	11820	11830	11840 1185	50
794	GAAGGTA	TATTCTCT	CTTTTTAGGA	AAGTAGTTAT.GG	TTCGTATATAGG	2603 all seg
					TTCGTATATAGG TTCGTATATAGG	
800	GAAGGTAO	TATTCTCT	CTTTTTAGGA	AAGTAGTTATGG	TTCGTATATAGG	a909 all.seq
				_	-	
•		11860		44000	TAGTACCATGAA	Majority
844	CTACCCAA		11870 T.T.C.C.T.C.A.G.A.T.		11890 1190	0
					TAGTACCATGAA TAGTACCATGAA	
•			A LOUI-CACAI.	I A CAICTAUAGA	TAGTACCATGAA	a909_a11.seq

WO 2006/078318 Alignment Report of Al-1_alignment, using J. Hein method with Weighted residue weight table. Thursday, July 29, 2004 5:46, P.M., ... TTTTGCTTATATGACCAATAT Majority 11910 11920 11930 11940 11894 TTTTGCTTATATGACCAAGTAAAGTGAGGATATACTAACAAATGAAATAT 2603_ai1.seq 11667 TTTTGCTTATATGACCAAGTAAAGTGAGGATATACTAACAAATGAAATAT 18rs21_a11.seq 11899 TTTTGCTTATATGACCAAGTAAAGTGAGGATATACTAACAAATGAAATAT cohl_ail.seq 11899 TTTTGCTTATATGACCAAGTAAAGTGAGGATATACTAACAAATGAAATAT cjb111_ai1.seq 11901 TTTTGCTTATATGACCAAGTAAAGTGAGGATATACTAACAAATGAAATAT nem316_ail.seq 11900 TTTTGCTTATATGACCAAGTAAAGTGAGGATATACTAACAAATGAAATAT a909_ail.seq TTATTATCGTATTTGTCCATTTTATCGAAAAGTTTGCATATTATCATTAT Majority 11960 11970 11980 11990 11944 TTATTATCGTATTTGTCCATTTTATCGAAAAGTTTGCATATTATCATTAT 2603_ai1.seq 11717 TTATTATCGTATTTGTCCATTTTATCGAAAAGTTTGCATATTATCATTAT 18rs21_ai1.seq 11949 TTATTATCGTATTTGTCCATTTTATCGAAAAGTTTGCATATTATCATTAT cohlail.seq. 11949 TTATTATCGTATTTGTCCATTTTATCGAAAGTTTGCATATTATCATTAT cjb111_ai1.seq 11951 TTATTATCGTATTTGTCCATTTTATCGAAAAGTTTGCATATTATCATTAT nem316_ail.seq 11950 TTATTATCGTATTTGTCCATTTTATCGAAAAGTTTGCATATTATCATTAT a909_ail.seq GTTTGATAAGATGCAAATATAATGATAGTAGGAGCTAAATATGGATATTT Majority 12020 12030 12050 11994 GTTTGATAAGATGCAAATATAATGATAGTAGGAGCTAAATATGGATATTT 2603_ail.seq 11767 GTTTGATAAGATGCAAATATAATGATAGTAGGAGCTAAATATGGATATTT 18rs21_ai1.seq 11999 GTTT GATAAGATGCAAATATAATGATAGTAGGAGCTAAATATGGATATTT cohi_aii.seq. 11999 GTTTGATAAGATGCAAATATAATGATAGTAGGAGCTAAATATGGATATTT cjbii1_aii.seq 12001 GTTTGATAAGATGCAAATATAATGATAGGAGCTAAATATGGATATTT nem316_a11.seq GTTTGATAAGATGCAAATATAATGATAGGAGCTAAATATGGATATTT a909_ai1.seq 12000 AAAAATCAAGAGTATCCTAAGTGCTTTCCATTTTGAAATTCAAATATAG Majority 12060 12070 12080 12090 12100 12044 AAAAAATCAAGAGTATCCTAAGTGCTTTCCATTTTGAAATTCAAATATAG 2603_ail,seq 1817 AAAAAATCAAGAGTATCCTAAGTGCTTTCCATTTTGAAATTCAAATATAG 18rs21_ail.seq 2049 AAAAATCAAGAGTATCCTAAGTGCTTTCCATTTTGAAATTCAAATATAG cohl_ail.seq 2049 AAAAAATCAAGAGTATCCTAAGTGCTTTCCATTTTGAAATTCAAATATAG cjb111_ai1.seq 2051 AAAAAATCAAGAGTATCCTAAGTGCTTTCCATTTTGAAATTCAAATATAG nem316_ai1.seq 2050 AAAAAATCAAGAGTATCCTAAGTGCTTTCCATTTTGAAATTCAAATATAG a909_ai1.seq CTAATAGTTCTAGAACTTCTAATTGTTTTTCGTCGACGATATGAATTTTC Hajority 12120 12130 12140 -2094 CTAATAGTTCTAGAACTTCTAATTGTTTTCGTCGACGATATGAATTTTC 2603_ail.seq .1867 CTAATAGTTCTAGAACTTCTAATTGTTTTTCGTCGACGATATGAATTTTC 18rs21_ai1.seq 2099 CTAATAGTTCTAGAACTTCTAATTGTTTTTCGTCGACGATATGAATTTTC cohl_ail.seq 2099 CTAATAGTTCTAGAACTTCTAATTGTTTTTCGTCGACGATATGAATTTTC cjb111_ail.seq 2101 CTAATAGTTCTAGAACTTCTAATTGTTTTTCGTCGACGATATGAATTTTC nem316_ai1.seq 2100 CTAATAGTTCTAGAACTTCTAATTGTTTTTCGTCGACGATATGAATTTTC a909_ail.seq ATCTTAACTGTTAGGATTCCACCTCCCTTTGGTTAAAGAAAAAGGTCA Majority 12160 12170 12180

12190 12200 2144 AATCTTAACTGTTACGATTCCACCTCCCTTTGGTTAAAGAAAAAGGTCA 2603_ail.seq 1917 AATCTTAACTGTTAGGATTCCACCTCCCTTTGGTTAAAGAAAAAGGTCA 18rs21_ai1.seq 2149 AATCTTAACTGTTAGGATTCCACCTCCCTTTGGTTAAAGAAAAAGGTCA cohilai1.seq 2149 AATCTTAACTGTTAGGATTCCACCTCCCTTTGGTTAAAGAAAAAGGTCA cjbiii ali seq 2151 AATCTTAACTGTTAGMATTCCACCTCCCTTTGGTTAAAGAAAAAGGTCA nem316 aii seq 2150 AATCTTAACTGTTAGGATTCCACCTCCCTTTGGTTAAAGAAAAAGGTCA a909_a11.seq GGTCGTTTAGATAACTTTGTCAAACAAGCTCAAGCTATCTAAAAAAAGTT Majority

12210 12220 12230 .12240 12250 1967 CGTCGTTTAGATAACTTTGTCAAAGCTCAAGCTATCTAAAAAAATAGTT 18rs21_ai1.seq 2199 G'GTCGTTTAGATAACTTTGTCAAACCTCAAGCTATCTAAAAAATAGTT cohl_ail.seq 2199 GGTCGTTTAGATAACTTTGTCAAACAAGCTCAAGCTATCTAAAAATAGTT cjbii1.seq 2201 G G T C G T T T A G A T A A C T T T G T C A A A C A A G C T C A A G C T A T C T A A A A A A G T T nem316_a11.seq 2200 GGTCGTTTAGATAACTTTGTCAAACAAGCTCAAGCTATCTAAAAAATAGTT a909_ai1.seq

FIGURE 18 AH

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TGAAATCHEC.TOTACTTTTTTTATTAAGCTATCTGATGAGCAGAAGG Majority 12260 12280 12290 12300 12244 TGAAATGGGCATTACTCTAGTTTTTAATAAGCTATCTGATGAGCAGAAGG 2603_ai1.seq 12017 TGAAATGGGCATTACTCTAGTTTTTAATAAGCTATCTGATGAGCAGAAGG 18rs21_ai1.seq 12249 TGAAATGGGCATTACTCTAGTTTTTAATAAGCTATCTGATGAGGAAGG coh1_all.seq 12249 TGAAATGGGCATTACTCTAGTTTTTAATAAGCTATCTGATGAGCAGAAGG cjb111_ai1.seq 12251 TGAAATGGGCATTACTCTAGTTTTTAATAAGCTATCTGATGAGCAGAAGG nem316_ai1.seq 12250 TGAAATGGGCATTACTCTAGTTTTTAATAAGCTATCTGATGAGCAAAGG a909_a11.seq A G A A G T T A A T G C A T G T T G G G A A G T C T T A T T T T G A C T A T C A A G A A A T G C T Majority 12310 12320 12330 12340 12350 12294 A G A A G T T A A T G C A T G T T G G G A A G T C T T A T T T T G A C T A T C A A G A A A T G C T 2603_ail.seq 12067 AGAAGTTAATCCATGTTGGGAAGTCTTATTTTGACTATCAAGAAATGCT 18rs21_ai1.seq 12299 AGAAGTTAATGCATGTTGGGAAGTCTTATTTGACTATCAAGAAATGCT cohl_ail.seq 2299 A G A A G T T A A T G C A T G T T G G G A A G T C T T A T T T T G A C T A T C A A G A A A T G C T cjb111_ai1.seq 12301 AGAAGTTAATGCATGTTGGGAAGTCTTATTTGACTATCAAGAAATGCT nem316_ai1.seq 12300 AGAAGTTAATGCATGTTGGGAAGTCTTATTTTGACTATCAAGAAATGCT a909_ail.seq CTTATCCCACAATTAGGTTTTCTATATTCTAAATTAACTAAAAATTGA Majority 12360 12380 12390 12400 2344 CTTATCCCACAATTAGGTTTTCTATATTCTAAATTAACTAAAAATTGA 2603_ail.seq 2117 CTTATCCCACAATTAGGTTTTCTATATTCTAAATTAACTAAAAAAATTGA 18rs21_aii.seq 2349 CTTATCCCACAATTAGGTTTTCTATATTCTAAATTAACTAAAAAATTGA cohlai1.seq 2349 CTTATCCCACAATTAGGTTTTCTATATTCTAAATTAACTAAAAATTGA cjbiil_ail.seq 2351 CTTATCCCACAATTAGGTTTTCTATATTCTAAATTAACTAAAAATTGA nem316_ai1.seq 2350 CTTATCCCAAATTAGGTTTTCTATATTCTAAATTAACTAAAAAATTGA 2909_ai1.seq ACTTGATAATCGGTTGTCTCCGACTGAACAAAGTTATTGATTACCTTAT Majority 12420 12430 12440 12450 2394 A C T T G A T A A T C G G T T G T C T C C G A C T G A A A A A G T T A T T G A T T A C C T T A T 2603_ai1.seq 2167 ACTTGATAATCGGTTGTCTCCGACTGAACAAAGTTATTGATTACCTTAT 18rs21_ai1.seq 2399 ACTTGATAATCGGTTGTCTCCGACTGAACAAAGTTATTGATTACCTTAT coh1_ai1.seq 2399 ACTTGATAATCGGTTGTCTCCGACTGAACAAAGTTATTGATTACCTTAT cjb111_ai1.seq 2401 ACTTGATAATCGGTTGTCTCCGACTGAACAAAGTTATTGATTACCTTAT nem316_ai1.seq 2400 ACTTGATAATCGGTTGTCTCCGACTGAACAAAGTTATTGATTACCTTAT a909_ail.seq 12460 12480 12490 12500 ACCGATCTTTCTATACTAAACTTATATTGTTGCTTTAGAAATTTTAAAG Majority 12510 12520 12530 12540 12550 2494 ACCGATCTTTCTAAAACTTATTGTTGCTTTAGAATTTTTAAAG 2603_ai1.seq 2267 ACCGATCTTTCTATTCTAAAACTTATATTGTTGCTTTAGAAATTTTAAAG 18rs21_a11.seq 2499 ACCGATCTTTCTATTCTAAACTTATATTGTTGCTTTAGAAATTTTAAAG cjb111_a11.seq 2501 ACC.GATCTTTCTATTCTAAACTTATTGTTGCTTAGAAATTTTTAAAG nem316_a11.seq 2500 ACCGATCTTTCTAAAAACTTATTGTTGCTTAGAAATTTTAAAG a909_ail.seq AGCGTGGATGGCTTCATAATAAACAGAATCTTACCAATTTGCGAAGCCA Majority 12560 12570 12580 12590 12600 2544 A G C G T G G A T G C C T T C A T A A T A A A C A G A A A T C T T A C C A A T T T G C G A A G C C A 2603_ai1.seq 2317 AGCGTGGATGGCTTCATAATAAACAGAAATCTTACCAATTTGCGAAGCCA 18rs21_ai1.seq 2549 AGCGTGGATGGCTTCATAATAAACAGAAATCTTACCAATTTGCGAAGCCA cohl_all.seq 2549 AGCGTGGATGGCTTCATAATAAACAGAAATCTTACCAATTTGCGAAGCCA cjb111_ai1.seq 2551 A G C G T G G A T G G C T T C A T A A T A A A C A G A A A T C T T A C C A A T T T G C G A A G C C A nem316_ail.seq 2550 A G C G T G G A T G G C T T C A T A A T A A A C A G A A A T C T T A C C A A T T T G C G A A G C C A a909_ail.seq

ignment Report of Al-1_WO_2006/078318 ... Which is a superposition of the state of CT/US2005/027239 hursday, July 29, 2004 5:46 PM AAAAATAFFGATATTT GAAGETCCA TAGTCTAATAGATAGTCCAGTTAG Majority 12610 12630 12640 cohl_aii.seq 12660 12670 12680 12690 12700 2651 AGAAGCGTTGATTATAAGTGATAAGGATTTTCAAAAATTAAAACAAGAGC nem316_a11.seq 12710 12730 12740 12750 GATGATTC GGAAAAATAC GGAGACTATACTATTT CAAGGAAAAGATACAA Majority 12770 12780 12790 12800 2744 GATGATTCCGGAAAAATACGGAAGTATACTATTTCAAGGAAAAGATACAA 2603_ai1.seq 2517 GATGATTCGGAAAAATACGGAGACTATACTATTTCAAGGAAAAGATACAA 18rs21_ai1.seq 2749 GATGATTCGGAAAAATACGGAAGTATTACTATTTCAAGGAAAAGATACAA cohlait.seq 2749 GATGATTCGGAAAAATACGGAGACTATACTATTTCAAGGAAAAGATACAA cjb111_a11.seq 2751 GATGATTCGGAAAAATACGGAAGATACTATTCAAGGAAAAGATACAA nem316_ai1.seq 2750 GATGATTCGGAAAAATACGGAGACTATACTATTTCAAGGAAAGATACAA a909_a11.seq AAGTTTCGAATCAAGTCTTCAACTATACATCCTTCAAAGTCATCGCTAG Majority 12810 12830 12840 794 AAGTTTCGAATCAAGTCTTCAACTATACATCCTTCAAAGTCATCGCCTAG 2603_ail.seq 2567 AAGTTTCGAATCAAGTCTTCAACTATACATCCTTCAAAGTCATCGGCTAG 18rs21_ai1.seq 2799 AAGTTTCGAATCAAGTCTTCAACTATACATCCTTCAAAGTCATCGGCTAG cohl_ail.seq 2799 AAGTTTCGAATCAAGTCTTCAACTATACATCCTTCAAAGTCATCGCCTAG cjb111_ai1.seq 2801 A A G T T T C G A A T C A A G T C T T C A A C T A T A C A T C C T T C A A G T C A T C G G C T A G nem316_all.seq 2800 A A G T T T C G A A T C A A G T C T T C A A C T A T A C A T C C T T C A A G T C A T C G G C T A G a909_a11.seq A G A T T T G G A A T T A T G A A C C A A T C C C T T T G A T T A C T A G A A A A A A A A A G C Majority 12860 12870 12880 12890 12900 2844 A G A T T T G G A A T T A T G A A C C A A T C C C T T T G A T T A C T A G A A A A A A A A A A A G C 2603_ai1.seq. 517 AGATTTGGAATTATGAACCAATCCCTTTGATTACTAGAAAAAAATAACC 18rs21_ai1.seq 2849 A G A T T T G G A A T T A T G A A C C A A T C C C T T T G A T T A C T A G A A A A A A A A A A G C cohl_all_seq 849 A G A T T T G G A A T T A T G A A C C A A T C C C T T T G A T T A C T A G A A A A A A A A A A A A A G C cjbiil ail seq 251 AGATTTGGAATTATGAACCAATCCCTTTGATTACTAGAAAAATAGC nem316_at1.seq TTGGAGAGGCTAACGTGACACTGGTTGATCCAATCTCGCTTTATTAACA Wajority 12910 12920 12930 12940 12950

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Page 38

Alignment Report of Al-1_angnment, using J. Hern method with Weighted residue weight table.
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12717 CTAAGAATGAAGACCCTCGTATTGAAGAAGATTGAGCAGCTAGAA 18rs21_ai1.seq 12949 CTAAGAATGATGAAGACCCTCGTATTGAAGAAGATTGAGCAGCTAGAA cohl_all.seq 12949 CTAAGAATGATGAAGACCCTCGTATTGAAGAAGAAGTTGAGCAGCTAGAA Cjb111_ai1.seq
12951 CTAAGAATGATGAAGACCCTCGTATTGAAGAAGTTGAGCAGCTAGAA cjb111_ai1.seq 12950 CTAAGAATGATGAAGACCCTCGTATTGAAGAAGTTGAGCAGCTAGAA a909_ai1.seq GATAAGAT Majority

12994 GATAAGAT 12767 GATAAGAT 12999 GATAAGAT 12999 G A 13000 A 13000 GATAAGAT

2603_all.seq 18rs21_ai1.seq cohi_ail.seq cjblil_ail.seq nem316_ail.seq a909_a11.seq

Decoration 'Decoration #1': Shade (with solid black) residues that differ from the Consensus.

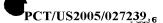
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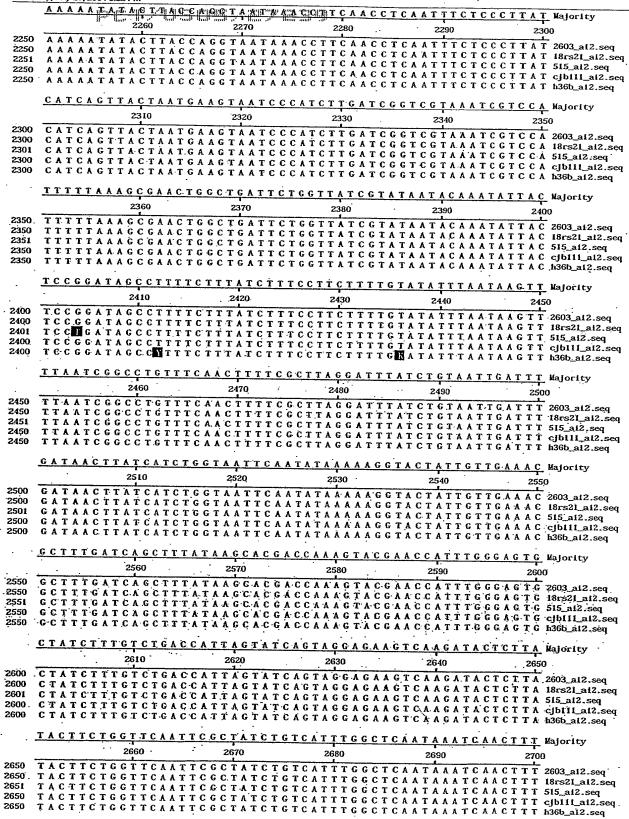
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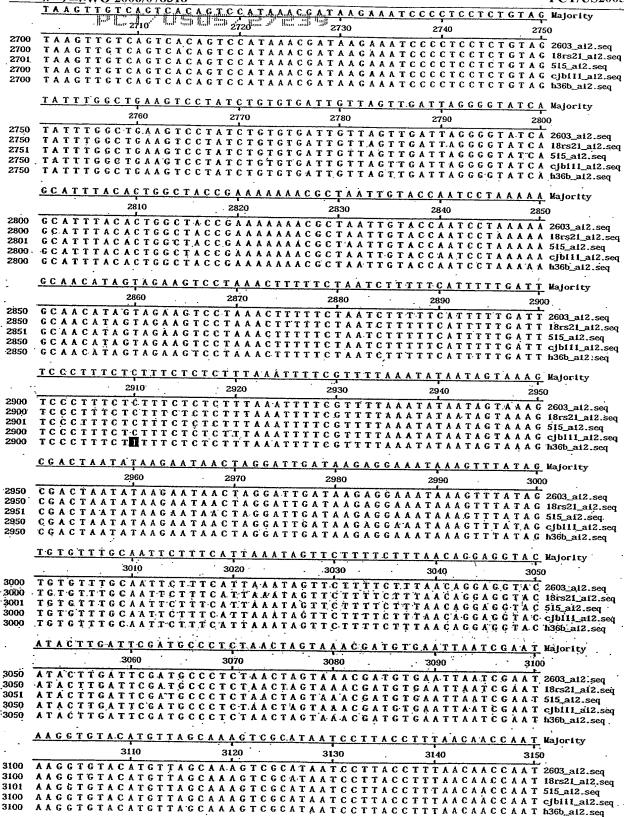
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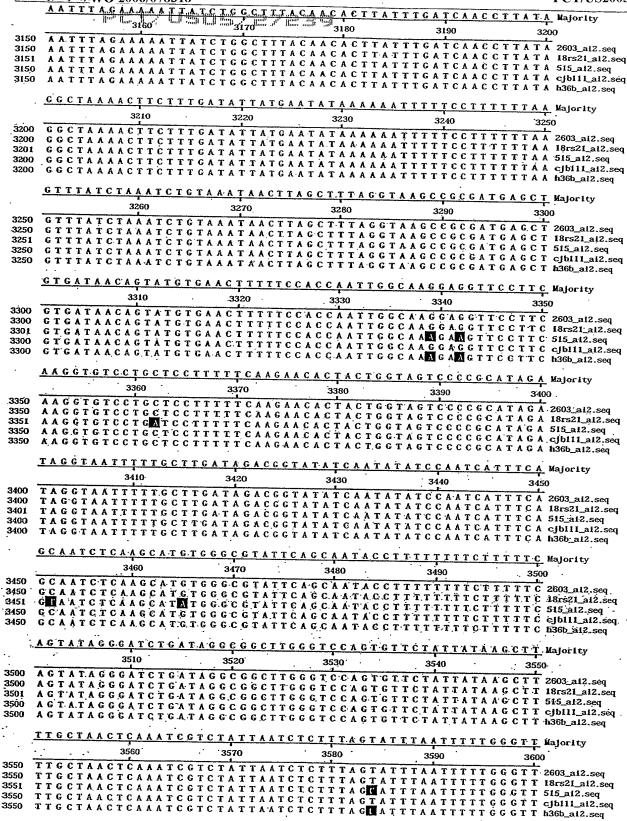
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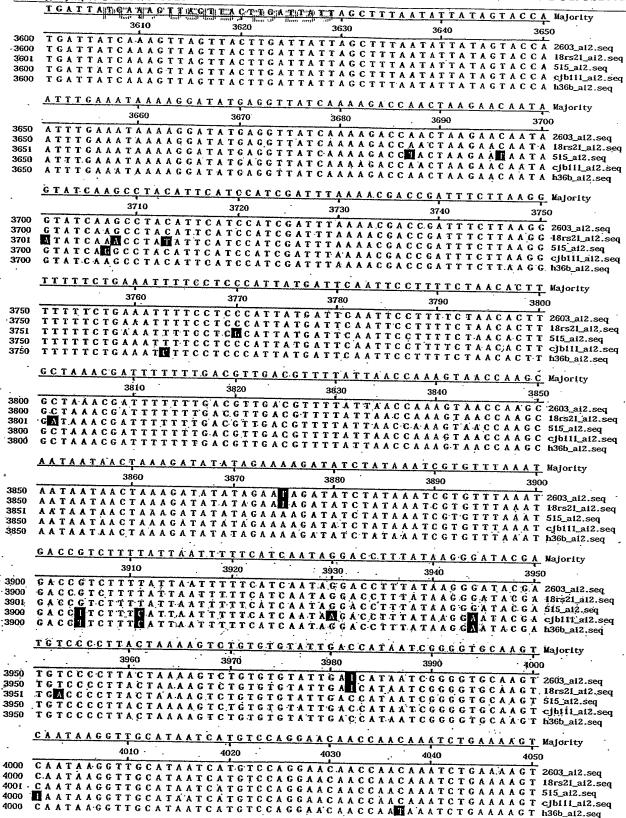
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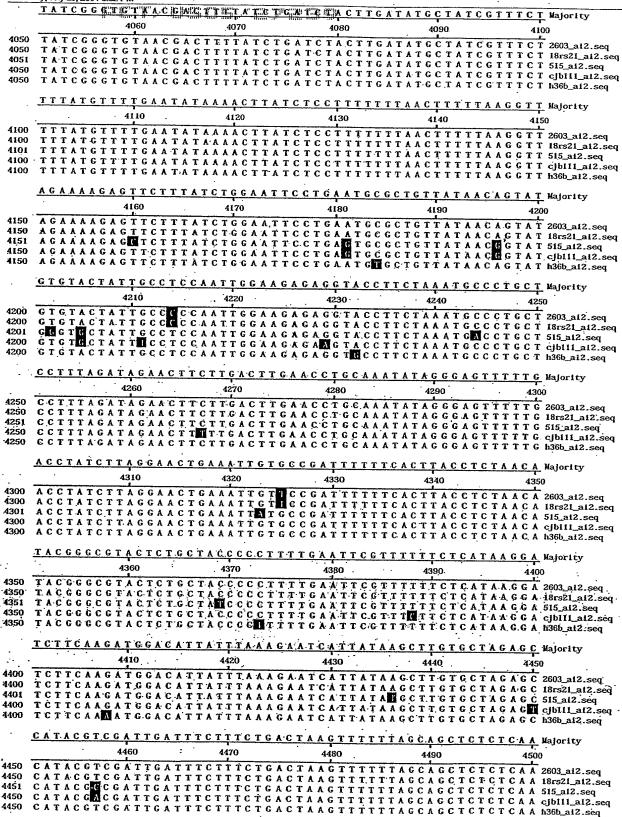


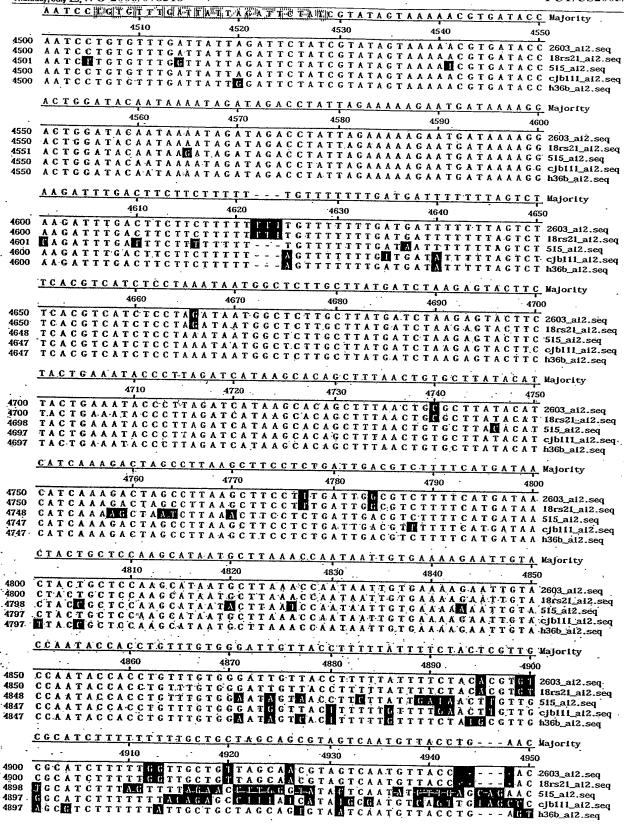


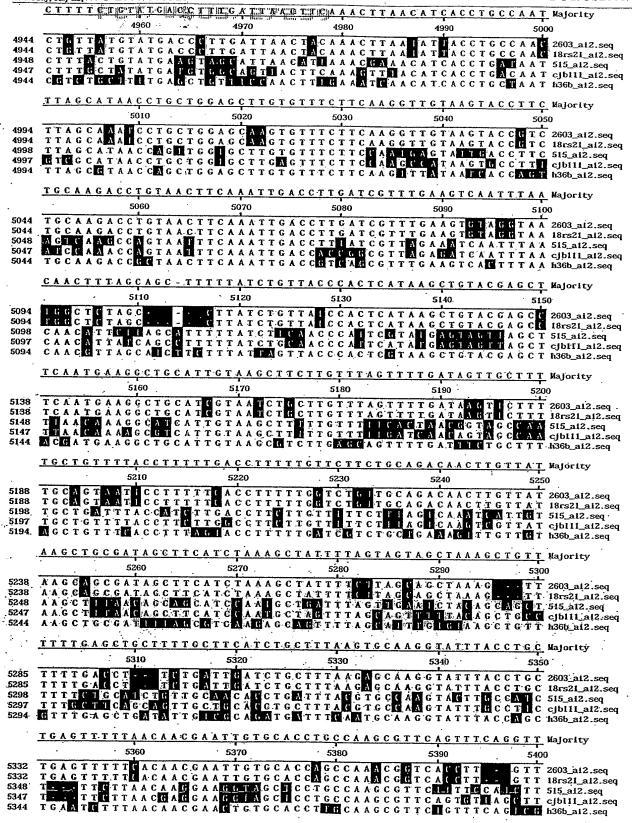


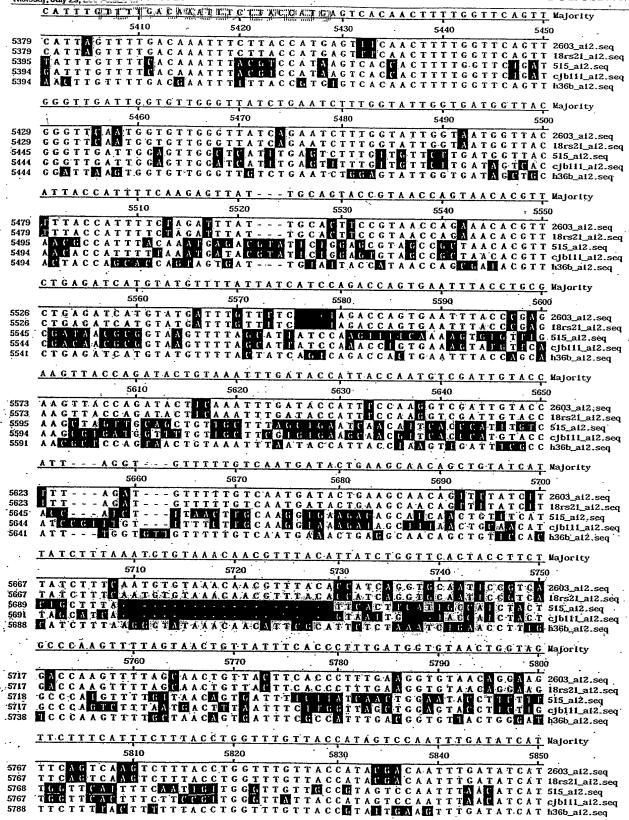


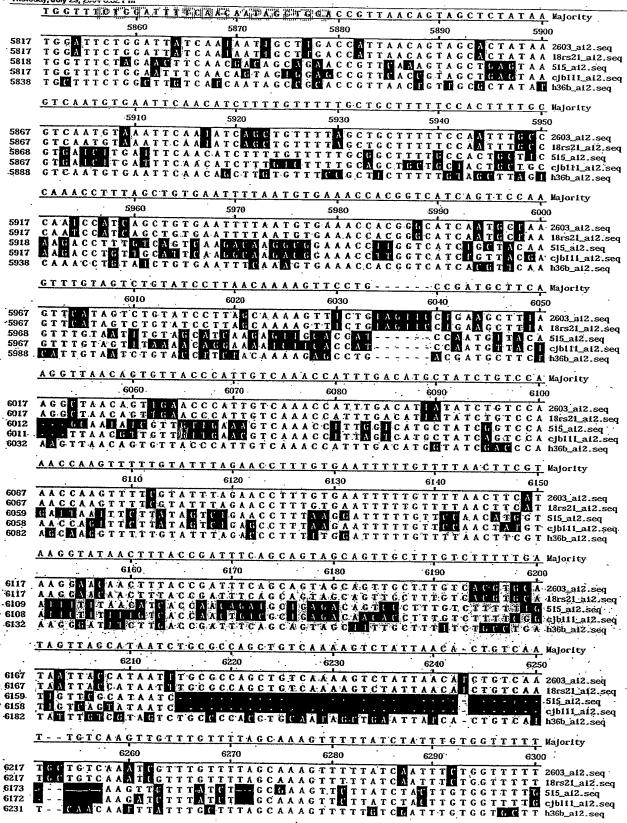


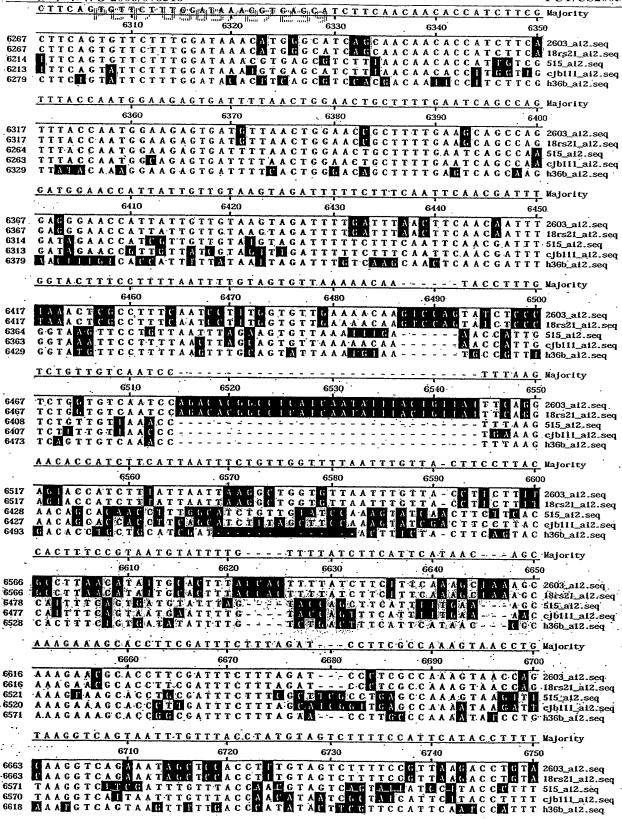


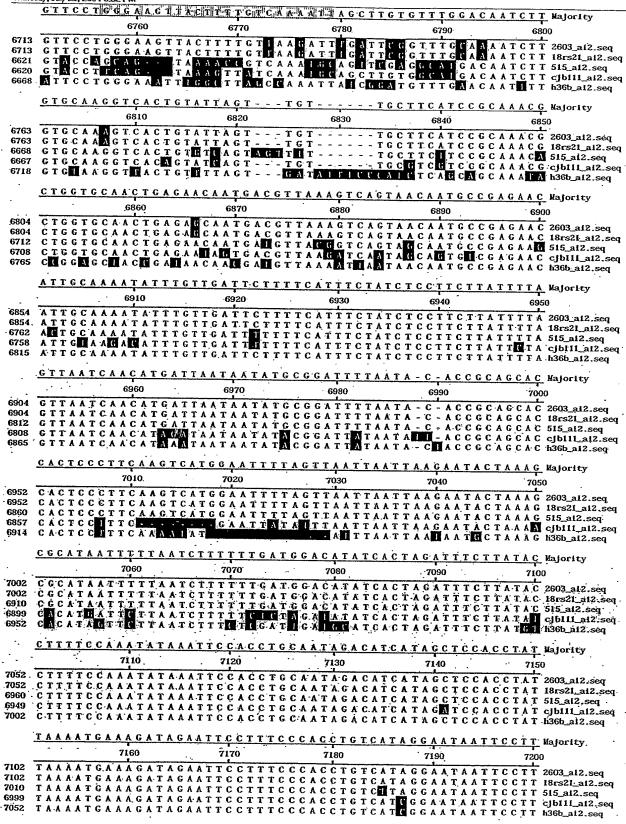


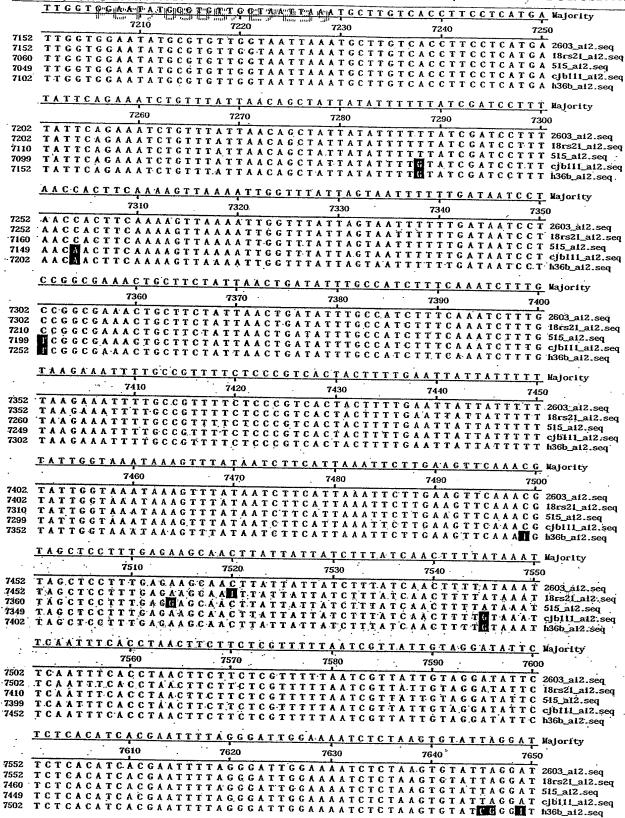


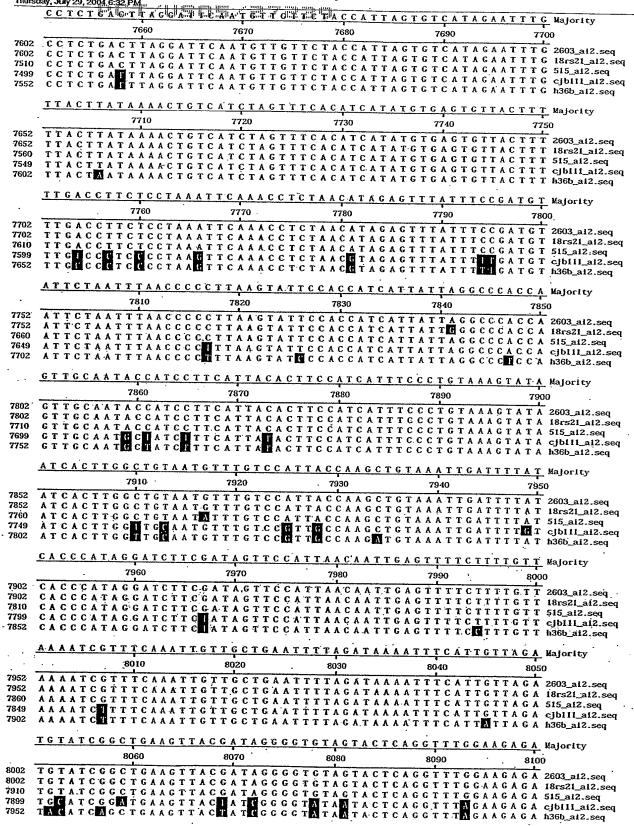


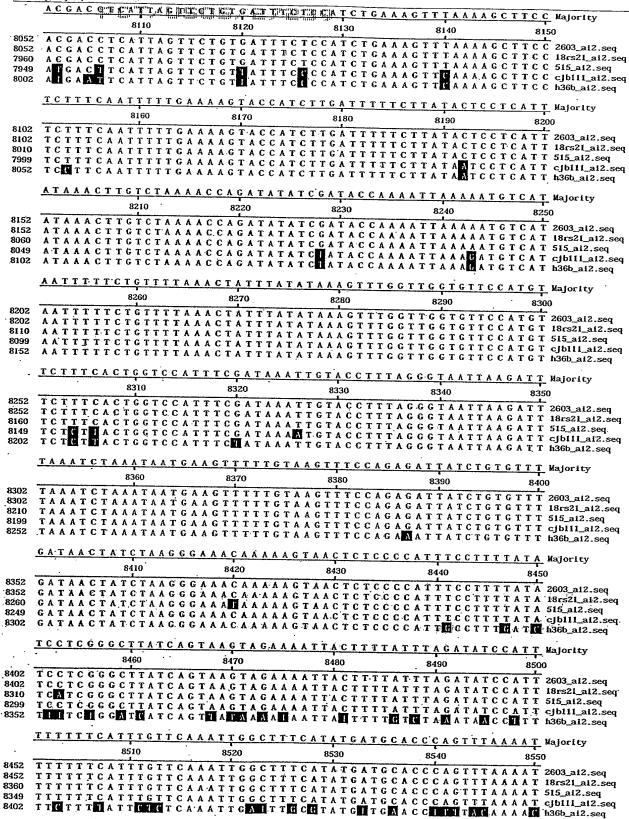


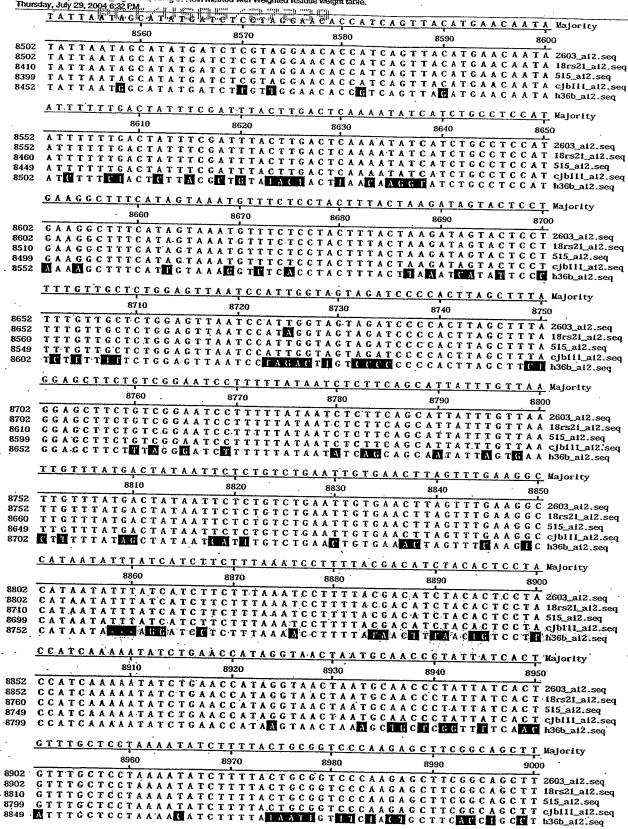


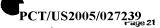


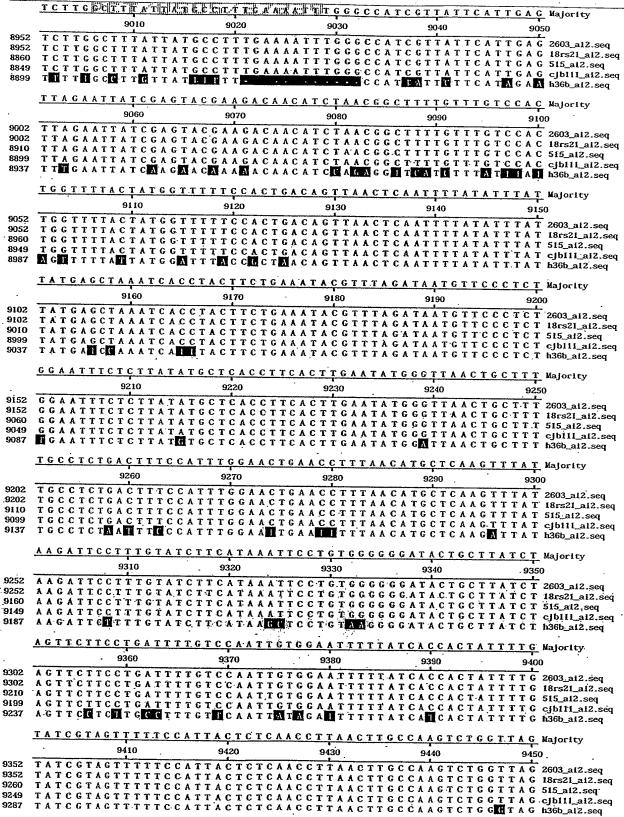


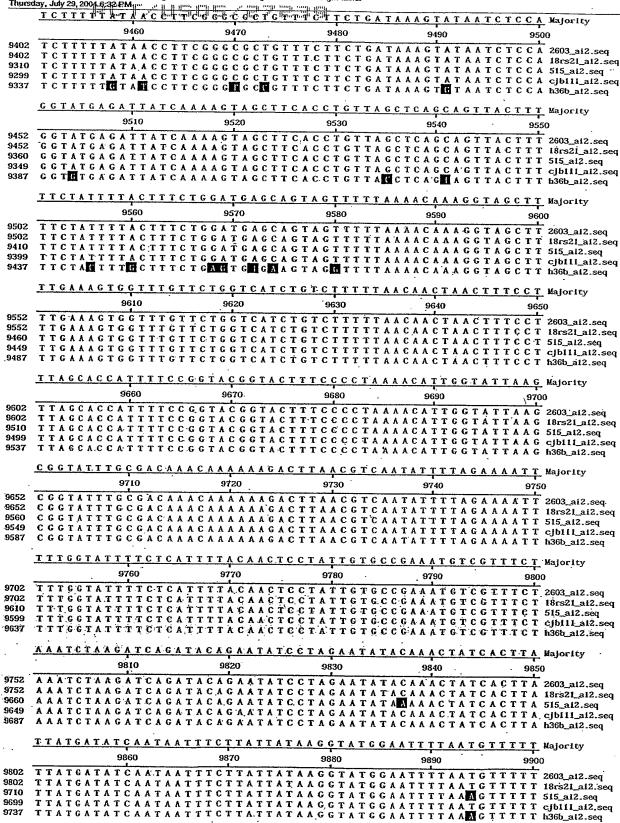


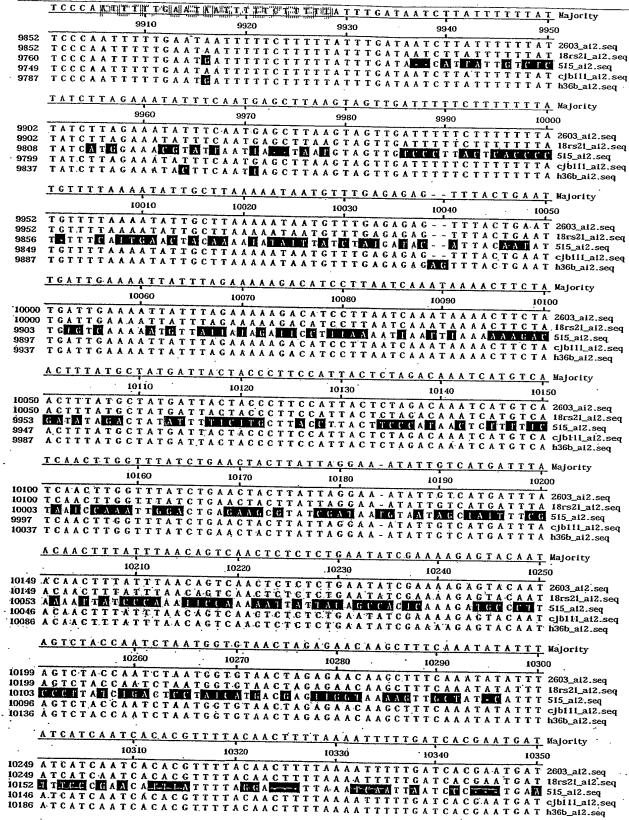


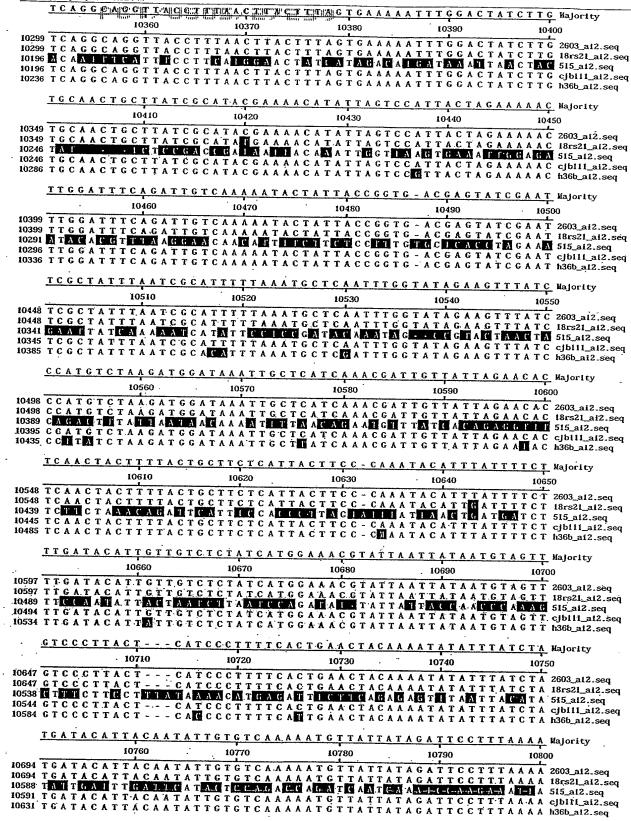


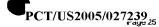


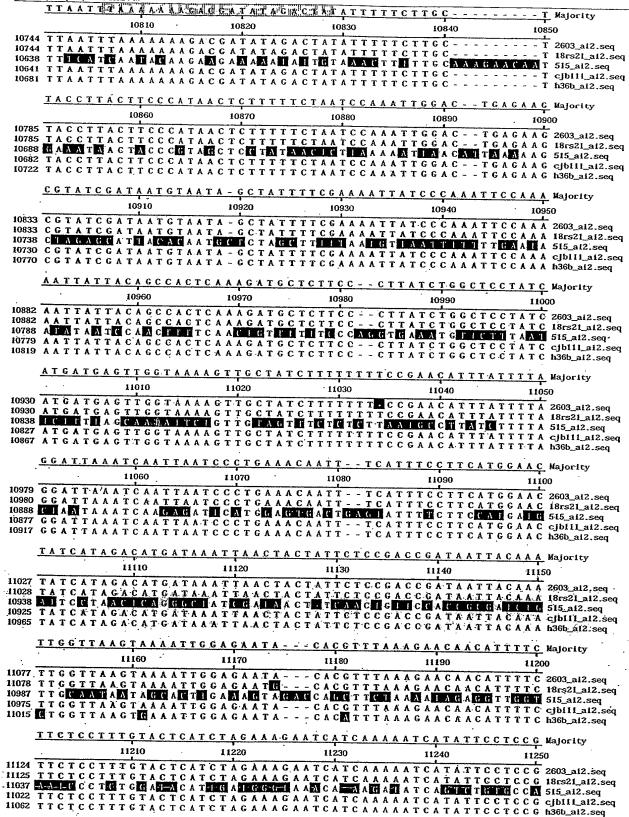


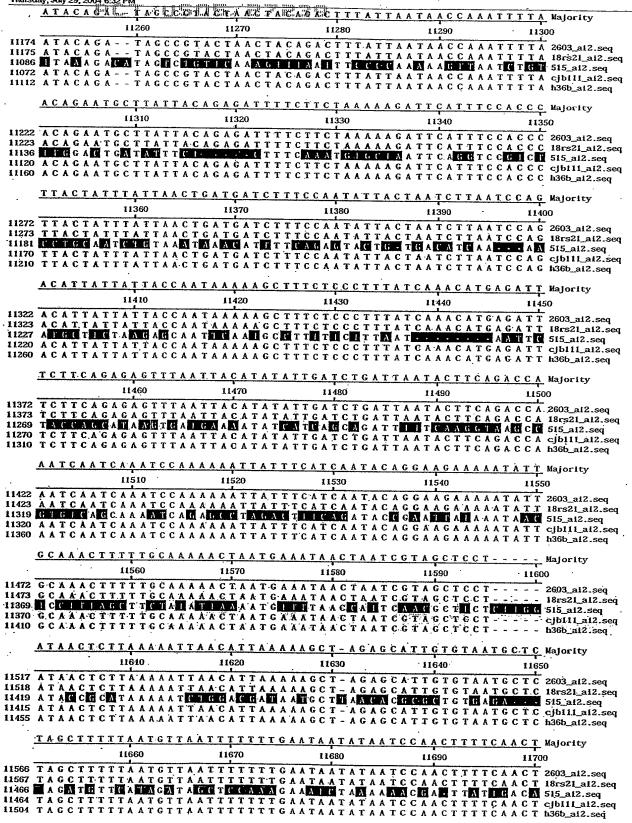


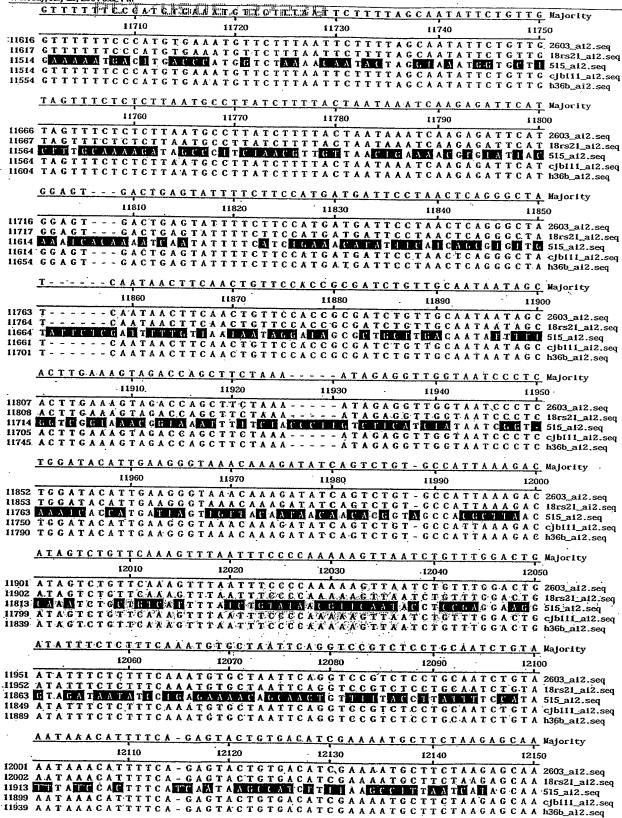




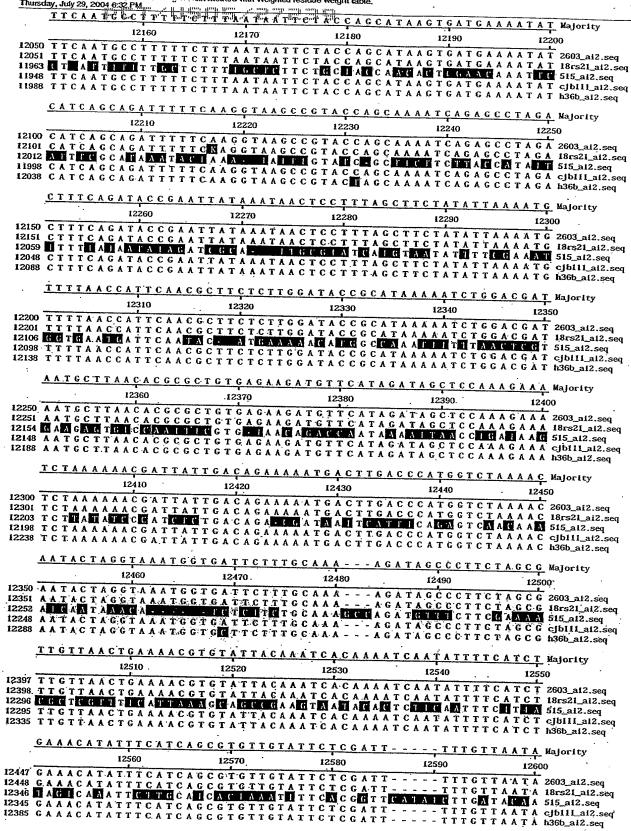


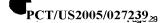


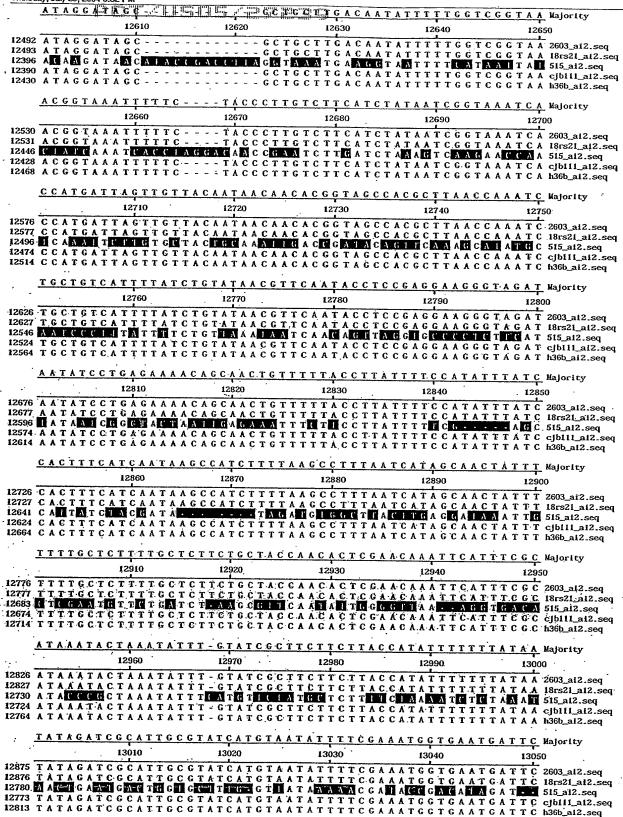




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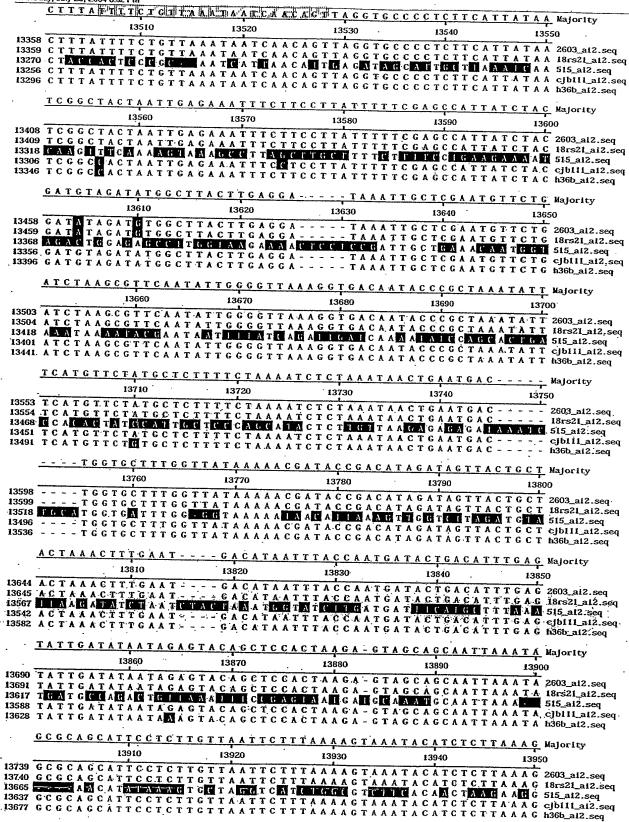






Page 30

•	AATAC	TG AAAA	ACATC	G C C A A	A program	TTAA	7 7 0 0 -			AAT Majorii	
		13060		13070		12000	LCGT	GAAGA	GTGTCC	AAT Majori	ty
12925	AATAC	ATGAAAA	ACATG		A T T T	13080		13090		13100	
12926	AATAC	ATGAAAA	ACATG	GCCAA	ATTT	I I I A A (TCGT	GAAGA	GTGTCC	13100 A A T 2603_at A A T 18rs21_	12.seq
12823	AATAC	A T C A 1 A	A A A	A D	ATLA	A A T-A	T	H A A H	UT UT UT	A A T 18rs21	_ai2.s
12863	AATAC	ATGAAAA	ACATG	GCCAA	ATTT1	T T A A (TCGT	GAAGA	GTGTCC	A A T 18rs21_ A I A 515_a12 A A T cjb111_ A A T h36b_a1	∴seq _ai2_s
f		TAACAG	ACCAA	TAAAA	TTAA-	- CCTG	ATAA	GTCTT	ATATCC	CAT Majorit	-17
12976	TTCGT	G T A A C A G	ACCAA	TAAAA	TTAA-	- CCTG	ATAA	G.T C T T	ATATCC	13150 C A T 2603_ai:	2
12877	TTGA	GTALLGA	T-A I A A	TAHAM	I A A A -	- CCTC	ATAA	GTCTT	ATATCC	C A T 2603_ai; C A T 18rs21_; A T 515_ai2	ai2.seq
	CTCTGA	CAGACG	ATAAT	CATT	CAGA	GTCAA	CAAA	ATCAA	T	C T Majority	
13023	CTCTGA	CAGACG	ATAAT	CATT	CAGA	GTCAA	CAAA		T 1 1 1 C 1	13200 F C T 2603_a12	
12001	CICIGA	CAGACG	A T A A T 7	CATTI	CAGA	GTCAA	CAAAA	ATCAA	rakaca; rakaca;	CT c]blli_a	ii2.se
9	CTTCTG	CAAAGC	CAGATO	тттст	TCGA		· • • • • • •			C A Majority	seq
13073	CTTCTG	CAAAGC	AGATO	TTTCT	TCCA			13240		13250 C A 2603_a12	
13074 (12973 (CTTCTG	CAAAGC	AGATG	TTTCT	TCGA	AAACG	CTCG1 CTCG1	TTTTC	TTAAAA	C A 2603_a12 C A 18rs21_a	.seq
12971	CTTCTG	C.A.A.G.C.C	AGMT	CATAT	A C G C	AGACA	A.T.A.A.A	TTCA	AAAA	C A 2603_ai2 C A 18rs21_a C 515_ai2.s	12.sec
13011 (CTTCTG	CAAAGCC	AGATG	TTTCT	TCAA	A A A C G :	CTCGT	TTTCA	TTAAAG	C A 18rs21_a C M 515_ai2.s C A cjbiii_a C A h36b_ai2.	i2.seq
	٠,	13260	<u> </u>	13270	I I,C T		TATA	GTCAA	ATTCT-	T G Majority	
13123 G	CCGAA	GTAATAC	ACTCT			13280		13290	· .	13300	
13124 G	CCGAA	GTAATAC	ACTCT	TCAAT	TTCT	1 1	LTATA	GTCAA	ATTCT-	13300 T G 2603_a12. T G 18rs21_a1	.seq
13023 G	CCCXA	EN LAATAM	CCC	ATAGE	ACCT	AAAFT	HH T A		ALICI	T G 18rs21_ai	l2.seq
13061 G	CCGAA	GTÄATAC	ACTCT	TCAAT	ттст. ттст.	7	TATA	GTCAA	ATTCT-	T G 18rs21_ai T J 515_ai2.s T G cjbiii_ai T G h36b_ai2.	2.seq
											seq
		13310	TCAC	GGITC.	ATATO	TTGAT	ACAA	ACAAG	ATAACA	TA Majority	:
13167 C	ATCAC	FAAATTT		10020		13330		13340		13350	
13168 C	ATCACI	TTTAAAT	- T C A C	G G T T C .	ATATO	TTGAT	ACAA	ACAAG	ATAACA	13350 T A 2603_ai2.s T A 18rs21_ai2	seq
13065 C	ATCACE		CAC	AALTC	AATA	AUTGU	AHAT	ACRAG	TAACA	I A 18rs21_ai2	2.seq
13105 C	ATMACI	TAAAT	- I C A C (GGTTCI	ATATC	TTGAT	ACAA	ACAAC	ATAACA	T A 18rs21_ai2 T	eq 2.sea
											seq
<u>~</u> .		13360	GGTAAA	TGAAG	GTAA	TTTTC	ATAA	<u> т</u>	TATCTAT	C Majority	
13217 C	C G	ACCTTA.	G-G T A A A	TGAAG	GTAA	TTTTC	ATAA	T	TATCTAT	13400 F.C 2603_a12.s	200
13154 C		ACCTTAC	GGTAAA	TGAAG	GTAA	TTTTC	ATAA	T	LATCATA	1 515_ai2.se C cjbiii_ai2	q
											eq
` <u>A</u> A	LATCAC	C T A G G A C	AACCG	AATCT	TGAT	CTAAA	GTCAA	GAACO	****	4 30 4 4.	•
13258 A A	LATCAC	CTAGGAC	AACCG	AATCT	TGAT	CTAAA			1 1 7 0 1 1	3450 A 2603_a12.se	
10150 A A	AICAC	CIAGGAC	AACCG	AATCT	TGAT	CTAAA	GTCAA	GAACO		A cjb111_a12.	.seq
TT	CTTGT	GCTACTG	CAAAT	TGACC	GATA	CACTT			_		ત્ર્યું.
	•	2	1.	7470		13/00				- ,	
13308 T T	CTTGT	GCTACTG	64445					13490	13	3500 C 2603_ai2.se	
13309 T T	CTTGT	GCTACTG	CAAAT	TGACC	GATA	CAGTT(. A A A G	CATAT	GCAAT	C 2603_ai2.se C 18rs21_ai2.	p:
·13246 T T	CTTGT	GCTACTG	CAAAT	TGACC	MATACA (GATAC	AGTTO	AAAG	CATAT	GCAATT	C 515_ai2.seq C cjbiii_ai2.se C h36b_ai2.se	seq
			•				AAAG	CALAT	G.C.A.A.T.T	C h36b_a12.se	q



	ÁGA	TAGC	Harry Author	الجاله الجان	TO THE RE	mar	ng make n								
		- A Min	111111111111111111111111111111111111111	A LIAIL	8 E. F.	RIA, G A	CATA	TAX	ATTC	AGT	AATA	ACTO	TAGA	GATA	Majority
			13960			13970			13090	1		****		•	
1378	9 A G A	TAGC	TTC	TIT	1.00							13990		140	
1379	AGA	TAGC	TTC	12 11 12 . 1 17 1 17	A G G (GAGA	CAA	TAA	ATTC	AGT	AATA	ACTO	GTAGA	GATA	2603_ai2.seq 18rs21_ai2.sec
13/1												ALI	. I A G A	CATA	18rc21 a12
1.000	/ A (+ A	T A C C	T T C 4	1 ~ 4 ~											515 012 000
1372	7 AGA	TAGC	TTC	T A 72	A GENT	AGA	CAA	TAA	ATTC	AGTA	ATA	ACTO	TAGA	GATA	515_a12.seq cjb111_a12.seq
	-			vens		AGA	CAA	TAA	ATTC	AGT	AATA	ACTO	TAGA	GATA	cjbili_ai2.seq h36b_ai2.seq
	ATA	GCTC	CCAT	AGC			4 T T								
						AAA	AII	G G T	ATTA	AAAC	TAT	ATTA	AGCA	CAAC	Majority
•			~ ***	•		14020			14030					-	
13839	ATA	GCTC	CCAT	AGC	CCT	· A A A	4 T T	CCT	1.7.7.4					1405	
13840	ATA	GCTC	CCAT	AGCA	CCT		ATT	C.C.A.	AIIA	AAAG	TAT	ATTA	AGCA	CAAC	2603_ai2.seq 18rs21_ai2.seq
13/5/							. 1885				, , , ,		AGLA	1: A A C	19~~21 ~12
13/3/		CCTC	ccar									AL AL A		CASHERI	515 212 222
13777	ATA	GCTC	CCAT	AGCA	CCT	AAA	ATT	CCT	A T T'A	AAA	TAT	ATTA	AGCA	CAAC	cjbiii_ai2.seq
										" " I O		WILW	AGCAI	CAAC	h36b at2 sea
	ATT.	TGCC	ACAA	GTCC	AAT	AAC	TGC	LGA	CATT	CTCT		4.0	CTTT		-
			14060			14000				0 1 0 1	<u> </u>	A G	CTTT	CTA	Majority
12000						14070			14080			1 4000			
13889	ATT	TGCC	ACAA	GTCC	AAT	AAC	TGC	GA	CATT	GTGT	Α .	1.6	C T T T		
13890	ATT	rgcc.	ACAA	G T C C	AAT	A A C.	TGC	L G A	CATT	GTCT	Α	A G	CTTT	CTA	2603_a12.seq 18rs21_a12.seq
13002		A CHA C	H C A	ATAA	ATT	A A	A C C	1 (ATT	AAAT	A HA			GTA	18rs21_ai2.seq 515_ai2.seq
13027	A T T		ACAA	GTCC	AAT	AAC'	TGCA	GA	CATT	GTGT	A ~ -	A C	CTTT		515_ai2.seq cjb111_ai2.seq
13027	v r'r .	I G C C	ACAA	GTCC	AAT	AAC.	T G C A	GA	CATT	GTGT	A	A G	CTTTT	CCTA	cjb111_a12.seq h36b_a12.seq
	CCTC												CILLI	GIA	n36b_a12.seq
	U U I U	. 1 1 6 /	AAGC	CAGT	AGA	TACT	GTG	TC	CTA	AAGC	GTT	ACCA	TAAGA	AAT	Valanten
			14110			14120			14130					•	
13935	CGTC	TTC	AACC	CACT	4.6.4	7.40						14140		14150	
13936	CGTC	TTG	LAGO	CAGI	AGA	TACT	CTC	TC	CTA	AAGÇ	GTT	ACCA	TAAGA	AAT	2603_ai2.seq 18rs21_ai2.seq
13852	CCT	TENEST A		4 0 0						· · · · ·	O 1 1	льск	LAAGA	AAT	18rc21 al2 aca
13833	CGTC	: T T C /	1 1.0	CACT		m				THE THE		U CELA	U A D A	I A EGGS	515 at2 coa ·
13873	CGTC	TTG	AGC	CAGT	AGA	1 A C 1		TOO	CTA	AAGC	G. T T	ACCA	TAAGA	AAT	515_a12.seq cjb111_a12.seq
										AAGÇ	GTT	ACCA	TAAGA	AAT	cjb111_ai2.seq h36b_ai2.seq
	GCAA	ATGA	TCA	TCAA	AGA	CTCA	A.C.								
		'	14160			•					- A C (GAU	AACTT	CAT	lajority
12005						14170		·	14180			14190	-	14200	i '
13985	GCAA	A T G A	TCA	T			-				-				•
12002	CVA	ATGA	T.C.A	T toest	<u> </u>					<u>-</u>	-				2603_a12.seq
13803	CCAA	AAA	THE	TAÄT	A C A	A C 1 A	Ă II				- C C	10 71 4	AAAA		8rs21_ai2.seq 15_ai2.seq
13923	CCAA	ATGA	TCA	CAA.	A G A (CTCA	A CA	G C t	A 1 1 A	G U G	HACC	GAC	AACTT	CAT	15_ai2.seq :jb111_ai2.seq
	O C A A	A I G A	ICA	L C A A	AGAG	CTCA	A CA	G C C	A-1 1 A	GCG	ACC	GAC	ARCTT	CATE	Jb111_ai2.seq 36b_ai2.seq
	ACCC	TTTC	C.C.A.4								-	•		·	Jou_arc.seq
•		~ ~ , ~ ∪	CCAS	HAAA	A G A. A	GAC	- G C	<u>A</u>	A	AXXX	XXX	XXXX	xxxx	xxx	alority
			14210		1	14220			14230			4240		•	-39
13997						سنناه	C		A			1210		14250	
13998								A	A	. А				2	603_ai2.seq
13940	A C	1 1 1	1 A 18	(- 10	7 1 1 1	4 4 6								1	8rs21 at2 con
13933	A C C C	TTTC	CCAA	AAA	GAA	GAG	G C	4 4		MAN A A	166	A + C	1 4 5 6	A I I 5	8rs21_ai2.seq 15_ai2.seq
13973	ACCC	TTTC	CCAA	AAAA	GAA	GAC	GC	A	· A	A	• 4 A A	C ((TACC	A C	jbiii_ai2.seq
•						,			A	Α .		•		h	36b_ai2.seq
2	XXXX.	xxxx	XXXX	XXXX	XX			•							
			14260									•		M	ajority
14000 -													-		
14000	•												•	•	203, -10
				<u> </u>									••	- 21	603_a12.seq
13983		1 A	1. 9 9 9	G A I A	<u> </u>									1	Brs21_ai2.seq
13963 <u>I</u> 14000		(4 4 1	4	v v (, v	الجيد				,			•			15_a12.seq
		. ,		· • · · · ·						•					bili_ai2.seq
														n	6b_ai2.seq

Decoration 'Decoration #1': Shade (with solid black) residues that differ from the Consensus.

Align	30dy, July 23, 2004,0.	49.EM	ain method with Weighted r	•	PCT/US2005
	GTTGCTT	C.A TAA C.T	LETC T G'A A G'G	C.T.A. TTCTAAAGTCAC.	A T G C A T T C T Majority
		10	20	30 40	50
I	GTTGCTT	CATAAGT	TGTCTGAAGG	CCTAATTCTAAAGTCAC	A T G C A T T C T nem316_a12.seq
	TTCAGAA	AGTTCAG	GAGATAGTAT	TATAGTTTCATCAGGTA.	••
2		60	70	80 . 90	100
2 .51	TTCAGAA	AGTTCAG	GAGATAGTAT	TATAGTTTCATCAGGTA	A G C A A T C C G nem316 a12.seq
				TAACTCCTGGCTCATTA	•
		110	120	130 140	150
2 101	G C C T T G T G C C T T G T	T C C G A T G T	T T G A T T C C G A 1 T T G A T C C G A 1	TAACTCCTGGCTCATTA. TAACTCCTGGCTCATTA.	A TAGCCTGT 2603_a12.seq
				ACTTAGCATGGGTATT	
		160	- 170	180 190	.200
52 151	T C G T A A C T C G T A A C		ATTATCTCTA ATTATCTCTA	A C T T A G C A T G G G T A T T C A C T T A G C A T G G G T A T T C	G G T A A A A T T 2603_at2.seq
	TTGAAAA			ACCTCGGGCCÁCTTCT	
		210	220	230 240	250
102 201	T T G A A A A T T G A A A A	TAGACTAA TAGACTAA	GTATTTATTA		TATGCATGA 2603_ai2.seq
				ACGAATAGGAGCTTCTG	TATGCATGA nem316_at2.seq
		260	270	280 290	300
152 251	AATCAAT	T T C T T T A T	AGAATTGTTC	A C G A A T A G G A G C T T C T C A C G A A T A G G A G C T T C T C	C A C C A A C T 2002 -12
				TGCAAAAGTGCATCCT	
. :		310	320	330 340	350 Majority
202 301	ATAGCAT	CCCCTGAA	CCAGAAACTG	TGCAAAAGTGCACCCT	. C.C.T.C.T.L.C.C.
· .			•	TGCAAAAGTGCATCCT	
		360	370	T C A A A A C C A G C A T C T A T 380 390	AGGTAATT Majority
252 351	A A C T G T T	C C G T C T C T C C G T C T C T	GTTAGGACAG GTTAGGACAG	T C A A A A C C A G C A T C T A T T C A A A A C C A G C A T C T A T	1 C C T A A T T 2000 10
				TCGATAATAATCATTAA	
,		410	. 420	430 440	. 450
302 401	TAAATAT	T T T T T C T C T T T T T C T C	CAAAGAGTTC CAAAGAGTTC	T C G A T A A T A A T C A T T A A T C G A T A A T A A T C A T T A A	TCGCACGA 2603_ai2.seq
				ATCACAATTTTAACTAA	
		460	470	480 490	500
352 451	TAACGTTT	T T T T C A T A	G G A T A A T T G T G G A T A A T T G T	A T C A C A A T T T T A A C T A A A T C A C A A T T T T A A C T A A	AATAACCT 2603_ai2.seq
				ATTGGAACGTCAGTTAG	
		510	520	530 540	550
402 501	CACTACTACTA		A C T A A A A A G A C T T A A A A A G	ATTGGAACGTCAGTTAG ATTGGAACGTCAGTTAG	TCCCAATC 2603_a12.seq .
			• •	CAATCCTTGGCTAAAAA	•
		560	570	580 590	GATATAC G Hajority
452 551	TTTTATTT TTTTATTT	A C T T C A C	TTTCTTTAAC TTTCTTTAAC	C A A T C C T T G G C T A A A A A C A A T C C T T G G C T A A A A A	CATATACC 2000 10 1
•				AAGTATAAAACCAGCTA	
		610	620	630 640	650
502 601	C A G T T A G A C A G T T A G A	TTCAAAA	TACCATAAGC TACCATAAGC	A A G T A T A A A A C C A G C T A A A G T A T A A A A C C A G C T A	1 1 1 0 1 7 0 7 0000
	-				AAAUHIUI NEMBIB AIZ SAA

	nment Report CY Q_2000/0, 70310 instay, July 29, 2004-6:46 PM;	fein method with Weighted n	esidue weight table.		FC1/US2003/0.
	GTCGGAAA"ATGAA"C	CCTAGGTXAX	II 111 111 1111 1111 1111 1111 1111 11	CCCAATTALL	
	660	670	680	C C C A A T T A A A	
552		CCCTAGGTAAA	TACCACATA		700
651	GTCGGAAATGAAC	CCCTAGGTAAA	TACGAGATAA	CCCAATTAAA	AAAA 2003_a12.seq AAAA T nem316_a12.seq
	GAGCAAACCCAAAG	TACCTTGGCAC	AACAGTTTCC	ATATACTETT	A G G C A Majoritus
	710	720	730	740	750
602 701	G A G C A A A C C C A A A G G A G C A A A C C C A A A M	TACCTTGGCAC	AACAGTTTCC	ATATACTCTT	A G G C A 2603_a12.seq
			KKCKGIIIEC	ATATACTCTT	AGGCA nem316_a12.seq
	TATAGTACTGCAAT	AAATAATAAT	ACTCCCAAAT	ATCATAAATG	TCCC Majority
652	760	770	780	790	800
751	TATAGTACTGCAAT	* * * * * * * * * * * * * * * * * * *	ACTCCCAAAT ACTCCCAAAT	ATCATAAATG	TTCCC 2603_ai2.seq
	ATCGAGTGCCCACT	GGGAAACCAAT	100010000		in the memoria ara.seq
	ATCGAGTGCCCACT	820	830		•
702	ATCGAGTGCCACT	GGGAAACGAAT	1000000000	840	850
108	ATCGAGTGCCCACT	GGGAAACGAAT	AGCCACCTGC	AAATACTAAA	GGGT nem316_ai2.seq
	TAAAGTTGGTCTTAC				
	860	870	880	890	900
752 851	TAAAGTTGGTCTTAG	TCTTTGAAAA	ATAAGTTTTA	AAGAAAGTATA	<u>i</u> .
			KIKKGIIIIK	AAGAAAGTATA	CATA nem316_a12.seq
	TACCAGAGATAATAG		GATAAATCTA	G C T T G A G G A T A	CCAC Majority
802	910 TACCACACATATA	920	930	940	950
901	TACCAGAGATAATAC TACCAGAGATAATAC	CATTTACTGC	G A T A A A T C T A . G A T A A A T C T A .	G C T T G A G G A T A G C T T G A G G A F A	C C A C 2603_ai2.seq
	TTCTTAAGGTAACAG				
٠.	960	970	980	990	1000
852 951	TTCTTAAGGTAACAG	AAAGTGACGC	T:CATAATCGC		 .
001			ICATAAICG:CI	AATAGCTATCT	GGCT nem316_ai2.seq
•	TACAGTATTACCAAT	CACAGTGATT	AACTTGAAAAA	T C T T G T A G A A	AGAT Majority
902	TACAGTATTACCAAT	1020	1030 -	1040	1050
1001	TACAGTATTACCAAT	CACAGIGATT	A A C T T G A A A A A A A C T T G A A A A A	A T C T T G T A G A A A T C T T G T A G A A	A G A T 2603_ai2.seq
	TTGGCAACTGTCCTC				
	1060	1070	1080	1090	•
952	TTGGCAACTGTCCTC	TAACACTTTCT	FTCAATOOTT		1100 A A T T 2603 012 000
1051	TTGGCAACTGTC.CTC	TAACACTTTO	TTGAATGTTT1	GGTCAAATGC	A A T T nem316_ai2.seq
	ACAGTGTCGGGCCAA	TATTGATGAC	CAATCCTAAA	CTGAAAAATA	AGAT Majority
1000	1110	. 1120	1130	1140	1150
1002	A C A G T G T C G G G C C A A A C A G T G T C G G G C C A A	TATTTGATGAC	CAATCCTAAA	CTGAAAAATA	A G A T 2603_a12.seq
			THE COLUMN	OLGANARAIA	A G A I nem316_a12.seq
•	AATAGCAATAAATGC			ACGAGATAAC	ATTA Majority
1052		1170 T.T.C.A.A.T.A.A.C.T.T	1180	1.190	1200
1151	A A T A G C A A T A A A T G C A A T A G C A A T A A A T G C	TTGAATAAGTT	TACTATTTTG	ACGAGATAAC ACGAGATAAC	ATTA 2603_ai2.seq ATTA nem316.ai2.seq
	GTCTTTTTATATCTT				
	1210	1220	1230	1240	1250
1102	GTCTTTTTATATCTT GTCTTTTTATATCTT	TCTAATATTGG	CALLCALCOC	100711077	
1201		. O I K K I K I I G G	CAAACAAGCC	ACGTAAGTTA	GATA nem316_a12.seq.
	GAAAACAATC GAAAT				
	1260	1270	1280	1290	1300
1152 1251	G A A A A C A A T C G A A A T C G A A A T C G A A A T C G A A A T C G A A A T C G A A A T C G A A A T C G A A A T C G A A A T C G A A A T C G A A A T C G A A A T C G A A A A T C A A T C G A A A A T C A A T C G A A A A T C A A T C G A A A A T C A A A T C A A T C G A A A A T C A A T C G A A A A T C A A T C G A A A A T C A A T C G A A A A T C A A T C G A A A A T C A A T C G A A A A T C A A T C G A A A A T C A A T C G A A A A T C A A T C A A T C G A A A A T C A A T C A A T C A A T C A A T C A A T C A A T C A A T C A A A T C A A T C A A T C A A A T C A A T C A A T C A A A T C A A A T C A A T C A A T C A A T C A A T C A A A T C A A A T C A A A T C A A A T C A A T C A A A T C A A A T C A A A T C A A A T C A A T C A A A T C A A A T C A A A T C A A A T C A A T C A A A T C A A A T C A A A T C A A T C A A T C A A T C A A T C A A A A	T.A.A.A.A.T.T.C.C.T.T.A.A.A.A.T.T.C.C.T	CAACGATATT	AAATGGAATA	C C A 2603_a12.seq
			- unconinii	ARRIGGAATAI	NUCA nem316_at2.seq

	•			10/401	
Alignm	ent Report of Ar-2 3) 2006/078318 mynnen, using J. Hein met	nod with Weighted residue w		PCT/US2005/0
Himse	TTGTTAA	46 PM" , I JA" T T'G"	CTACACCAAT	AAATGTTCTGATATCAAAGT	T A Walnelty
		1310	1320	1330 1340	1350
1202 1301	T T G T T A A T T G T T A A	A A G G T A A T T G A A G G T A A T T G	C C T A C A C C A A T C C T A C A C C A A T	`	T A 2603_ai2.seq T A nem316_ai2.seq
	GCAAATA	• •	•	AGACATAGTTGAGAGCTACC	A T Najority
1252	C C 4 4 4 T 4	1360	1370	1380 1390	1400
1351	GCAAATA	TAGCATACAA	AGGAATEGCAA	A G A C A T A G T T G A G A G C T A C C A G A C A T A G T T G A G A G C T A C C	A T nem316_a12.seq
	AGATACG	•	•	AGACTAGCTTTAATAAAATC	
1302	ACATACC	1410 C.T.C.A.A.C.C.T.A.A.	1420	1430 1440	1450
1401	AGATACA	GTÇAĄGCTAA	CTGTACCAAAT	A G A C T A G C T T T A A T A A A A T C A G A C T A G C T T T A A T A A A A T C	TT nem316_a12.seq
.•	TTGCACT	•	•	AGCGAAACTTGCTAAAAATA	·
1252	TTOCACT	1460	1470	1480 1490	1500
1352 1451		CTCTCTATTT		A G C G A A A C T T G C T A A A A A T A A G C G A A A C T T G C T A A A A A T A	A A 2603_a12.seq A A nem316_a12.seq
	GCTAGAG		•	C G A T A A A G G T T T C T G G A C C A	C G Majority
1400		. 1510	1520	1530 1540	1550
1402	GCTAGAG	CAACCATATT	C	C A T A A A G G T T T C T G G A C C A C G A T A A A G G T T T C T G G A C C A	C G 2603_a12.seq .C G nem316_a12.seq
-	ATTAGCA	A G T A T A A C T T.	TAAAAGTGAT	CTTAATAAGAGTACACCATA	A C Majority
		1560	1570	1580 1590	1600
1452 1551	ATTAGCA	AGTATAACTT	Г Т А.А А А G.Т G А Т Г Т А А А А G Ț G А Т	C T T A A T A A G A G T A C A C C A T A C T A A T A A G A G T A C A C C A T A	A C 2603_ai2.seq A C nem316_ai2.seq
	TT.GATTT	CAAATCAAAT	A A A T A A A A G.C	A A C T A A C A T C G G A A G G A T T G	A A Majority
		1610	1620	1630 1640	1650
1502 1601				A A C T A A C A T C G G A A G G A T T G A A C T A A C A T C G G A A G G A T T G	
	AAATCAA	CCTTTAAAAAA	тстсстсстс	GTATTAATGGAAATGAAACC	A T Majority
	•	1660	1670	1680 1690	1700
·1552 1651				G T A T T A A T G G A A A T G A A A C C G T A T T A A T G G A A A T G A A A C C	
	CATCAAT	ACAAAGATAA	I G G C A G A A A G A	ATGGCGATTGTCACCATTTT	A C Majority
	<u></u>	1710	1720	1730 1740	1750
1602 1701				A T G G C G A T T G T C A C C A T T T T A T G G C G A T T G T C A C C A T T T T	A C 2603_a12.seq A C nem316_a12.seq
	GTGTATT	TGTCATAAAA	AATTCCTCCA	A.T.T.T.A.A.T.A.A.T.T.G.A.A.G.A.A	G C Majority
•		1760	1770	1780 1790	1800
1652 1751	G T G T A T T G T G T A T T	T G T C A T A A A A A A	A A T T C C T C C A A A T T C C T C C A	A T T T A A A T A A A T T G A A A G A A A T T T A A A T A A A T T G A A A G A A	G C 2603 at 2 seg
	TCCAAAG	G T A A G C G T A T C	TACGCGAAAA	AAACCTTTGTCTCTCCCAT	C C Majority
		1810	1820	1830 1840	1850
1702	TCCAAAG	G T A A G C G T A T	G T A C G C G A A A A	AA.CCTTTGTCTTCTCCCAT	C C 2603_ai2.seq
1801				A A A C C T T T G T C T T C T C C C A T C C A C A T C A G C T T T C G C T C G C	•
					1900
1751 1851	A G A C T T T A G A C T T T	ACTGTCGGTT	TGGAATCTCA	C C A C A T C A G C T T T C G C T C G C C C C A C A T C A G C T T T C G C T C G C	G G 2603_ai2.seq
		•		TGGAAGCGATTACCGCCGGT	-
		1910 .	1920	1930 1940	1950
1801	ACTGATG			TGGAAGCGATTACCGCCGGT	
				TEGAACCCATTACCCCCCCT	

Thurso	day, July 29, 2004 6:46 PM	
	GGAATTAOACCCTGCCCTCAAGACATAGCATAACAAAAAAACTTG Majority	
	1960 1970 1980 1990 2000	
1851	GGAATTACACCCTGCCCTGAAGACACCTATAGCATAACAAAAAAACTTG 2603_a12.seq	
1951	GGAATTACACCCTGCCCTGAAGACACCTATAGCATAACAAAAAACTTG zoo3_a12.seq	-a
		~1
	CAATT GCAAGTTTTTAATTACTAATTAGTAGTAGTGATTAAAAATCATA Majority	
	2010 2020 2030 2040 2050	
1901	CAATTGCAAGTTTTTAATTACTAATTAGTAGTAGTGATTAAAAAATCATA 2603_ai2.seq	
2001	CAATT GCAAGTTTTTTAATTACTAATTAGTAGTAGTAGTAATTAAAAATCATA nem316_a12.st	ģ≤
	TTAATACCAAATTACTATGCTGTATCGTTTCTTTCAGATTTGCTATTTTT Majority	
	2060 2070 2080 2090 2100	
1951	TTAATACCAAATTACTATACTGTATCGTTTCTTTCAGATTTGCTATTTTT 2603 ai2.seq	
2051	TTAATACCAAATTACTATGCTGTATCGTTTCTTTCAGATTTGCTATTTT nem316_ai2.se	∍q
	A G T T T T C T T A A A A A G A T A A A C A A A A T T C C C A A A A T A A T A C A A C C A A G A A Najority	
	2110 2120 2130 2140 2150	
200 I 210 I	AGTTTTTCTTAAAAAGATAAACAAAATTCCCAAAATAATACAACCAAGAA 2603_a12.seq	
2101	A-G T T T T T C T T A A A A A G A T A A A C A A A A T T C C C A A A A T A A T A C A A C C A A G A A nem316_a12.se	p c
	TTGTCAGTCCTCCACCAATAATCATTCCTGTTTTAGGAAGAATGATTGT Majority	
	2160 2170 2180 2190 2200	
2051	TIGICAGICCICCACCAATAATCATICCIGITTIAGGAAGAAATGATIGI 2603_ai2.seq	
2151	TTGTCAGTCCTCCACCAATAATCATTCCTGTTTTAGGAAGAAATGATTGT 2003_a12.seq	on.
•		~4
	GGAAAAAGCGGTTGTGATGGTTTAGGATTTGTTGGTGGAGGAGTTTCTTT Majority	
•	2210 2220 2230 2240 2250	
2101	GGAAAAAGCGGTTCTGATGGTTTAGGATTTGTTGGTGGAGGAGTTTCTTT 2603_a12.seq	
2201	GGAAAAACCGGTTGTGATGGTTTAGGATTTGTTGGTGGAGGAGTTTCTTT nem316_a12.sc	₽
	TT-CCTTTTCTACCTCTACTTCCTCTCTTTTTTTTTTCCALCCTCTCTTTTTTTT	
	TTCGTTTTCTACCTCTACTTCCTGTGTTTTATTAGCAACTACAGCAACTA Majority	
	2260 2270 2280 2290 2300	
2151	TTC GTTTTCTACCTCTACTTCCTGTGTTTTATTAGCAACTACAGCAACTA 2603_a12.seq	
2251 _.	TTCGTTTTCTACCTCTACTTCCTGTGTTTTATTAGCAACTACAGCAACTA nem316_at2.se	q
	CAGCATCCTTCATAGATATACGGTAACCAGTTAGTGCTTTTGCTTCTCGA Majority	
	2310 2320 2330 2340 2350	
2201	CAGCATCCTTCATAGATATACGGTAACCAGTTAGTGCTTTTGCTTCTCGA 2603_a12.seq	
2301	CAGCATCCTTCATAGATATACGGTAACCAGTTAGTGCTTTTGCTTCTCGA 2003, a12.seq	: 0
	·	-
	AAAATATACTTACCAGGTAATAAACCTTCAACCTCAATTTCTCCCTTATC Majority	
	2360 2370 2380 2390 2400	
2251	AAAATATACTTACCAGGTAATAAACCTTCAACCTCAATTTCTCCCTTATC 2603 ai2.seq	
2351	ААААТАТАСТТАССА G G ТААТАААССТТСААССТСААТТТСТСССТТАТС nem316_ai2.se	pç
	ATCAGTTACTAATGAAGTAATCCCATCTTGATCGGTCGTAAATCGTCCAT Majority	
	2410 2420 2430 2440 2450	
2301	ATCAGTTACTAATGAAGTAATCCCATCTTGATCGGTCGTAAATCGTCCAT 2603_a12.seq	
2401	ATCAGTTACTAATGAAGTAATCCCATCTTGATCGGTCGTAAATCGTCCAT nem316_ai2.se	:d·
	TTTTAAAGEGAACTGGCTGATTCTGGTTATCGTATAATACAAATATTACT Majority	
•	2460 2470 2480 2490 2500	•
2451	. TTTTAAAGCCAACTGGCTGATTCTGGTTATCGTATAATACAAATATTACT 2603_a12.seq TTTTAAAAGCGAACTGGCTGATTCTGGTTATCGTATAATACAAATATTACT nem316_a12.se	.~
. 2101	TITIA A GOODA GI GATIO I GOTTATO OTATA A TATA CA A A TATIA CI Hemsto_aiz.se	ત્ર
•	CCTGATAGCCTTTTCTTTATCTTTCCTTCTTTTGTATATTTAATAAGTTT Najority	
	2510 2520 2530 2540 2550	
2401	CCGGATAGCCTTTTCTTTATCTTTCCTTTTTTTTTTATATAACTAT 2603_a12.seq	
2501	CCTGATAGCCTTTTCTTTATCTTTCCTTCTTTTGTATATTTAACTTT 2003_a12.seq	ps
		•
•	TAATCGGCCTGTTTCAACTTTTCGCTTAGGATTTATCTGTAATTGATTTG Majority	
	2560 2570 ` 2580 2590 2600	
2451	TAATCGGCCTGTTTCAACTTTTCGCTTAGGATTTATCTGTAATTGATTTG 2603_a12.seq	
2551	TAATCGGCCTGTTTCAACTTTTCGCTTAGGATTTATCTGTAATTGATTTG nem316_a12.se	ю

WO 2006/078318 Alignment Report of Ai-2 alignment, using J. Hein method with Weighted residue weight Thursday, July 29, 200 646 PM Page 5 ATAACTTAT CATCTGGTATTTCAATATAAAAAGGTACTATTGTTGAAACG Majority ATAACTTATCATCTGGTAATTCAATATAAAAGGTACTATTGTTGAAACC 2603_ai2.seq ATAACTTATCATCTGGTATTTCAATATAAAAAGGTACTATTGTTGAAACG nem316_a12.seq CTTTGATCAGCTTTATAAGCACGACCAAAGTACGAACCATTTGGGAGTGC Majority CTTTGATCAGCTTTATAAGCACGACCAAAGTACGAACCATTTGGGAGTGC 2603_a12.seq CTTTGATCAGCTTTATAAGCACGACCAAAGTACGAACCATTTGGGGAGTGC nem316_a12.seq <u>T A T C T T T G T C T G A C C A T T A G T A T C A G T A G G A G A A G T C A A G A T A C T C T T A T</u> Majority TATCTTTGTCTGACCATTAGTATCAGTAGGAGAAGTCAAGATACTCTTAT 2603_a12.seq TATCTTTGTCTGACCATTAGTATCAGTAGGAGAGATACTCTTAT nem316_a12.seq ACTTCTGGTTCAATTCGCTATCTGTCATTTGGCTCAATAAATCAACTTTT Hajority 2651 ACTTCTGGTTCAATTCGCTATCTGTCATTTGGCTCAATAAATCAACTTTT 2603_a12.seq A C T T C T G G T T C A A T T C G C T A T C T G T C A T T T G G C T C A A T A A A T C A A C T T T T nem316_a12.seq AAGTTGTCAGTCACAGTCCATAAACGATAAGAAATCCCCTCTCTGTAGT Majority 2810-2701 AAGTTGTCAGTCACAGTCCATAAACGATAAGAAATCCCCTCCTCTGTAGT 2603_a12.seq A A G T T G T C A G T C A C A G T C C A T A A A C G A T A A G A A A T C C C C T C T C T G T A G T nem316_a12.seq ATTTGGCTGAAGTCCTATCTGTGTGATTGTTAGTTGATTAGGGGGTATCAG ATTTGGCTGAAGTCCTATCTGTGTGATTGTTAGTTGATTAGGGGGTATCAG 2603_a12.seq ATTTGGCTGAAGTCCTATCTGTGATTGTTAGTTGATTAGGGGGTATCAG nem316_a12.seq CATTTACACTGGCTACCGAAAAAACGCTAATTGTACCAATCCTAAAAG Majority CATTTACACTGGCTACCGAAAAAAACGCTAATTGTACCAATCCTAAAAAG 2603_ai2.seq CATTTACACTGGCTACCGAAAAAACGCTAATTGTACCAATCCTAAAAG nem316_ai2.seq CAACATAGTAGAAGTCCTAAACTTTTTCTAATCTTTTCATTTTTGATTT Majority CAACATAGTAGAAGTCCTAAACTTTTTCTAATCTTTTTCATTTTTGATTT 2603_a12.seq CCCTTTCTTTTCTCTCTTTTAAATTTTCGTTTTAAATATAATAGTAAAGC Majority CCCTTTCT TTTCTCTCTTTAAATTTTCGTTTTAAATATAATAGTAAAGC 2603_ai2.seq CCCTTTCTTTTCTCTCTTTAAATTTTCGTTTTAAATTTTAAATATAATAGTAAAGC nem316_ai2.seq GACTAATATAAGAATAACTAGGATTGATAAGGAAAATAAAGTTTATAGT Majority ·. . GACTAATATAAGAATAACTAGGATTGATTGATAAGGAAGTATAAAGTTTATAGT 2603_a12.seq GACTAATATAAGAATAACTAGGATTGATAAGAGAAATAAAGTTTATAGT nem316_a12.seq G T G T T T G C A A T T G T T T C A T T A A A T A G T T G T T T T C T T T A A C A G G A G G T A C A. Majority 3001 GTGTTTGCAATTCTTTCATTAAATAGTTCTTTTAACAGGAGGTACA 2603_ai2.seq GTGTTTGCAATTCTTTCATTAAATAGTTCTTTTCTTTAACAGGAGGTACA nem316_a12.seq TACTTGATTCGATGCCCTCTAACTAGTAAACGATGTGAATTAATCGAATA Majority 3051 TACTTGATTCGATGCCCTCTAACTAGTAAACGATGTGAATTAATCGAATA 2603_a12.seq

FIGURE 20D

TACTTGATTCGATGCCCTCTAACTAGTAAACGATGTGAATTAATCGAATA nem316_a12.seq A G G T G T A C A T G T T A G C A A A G T C G C A T A A T C C T T A C C T T T A A C A A C C A A T A Wajority

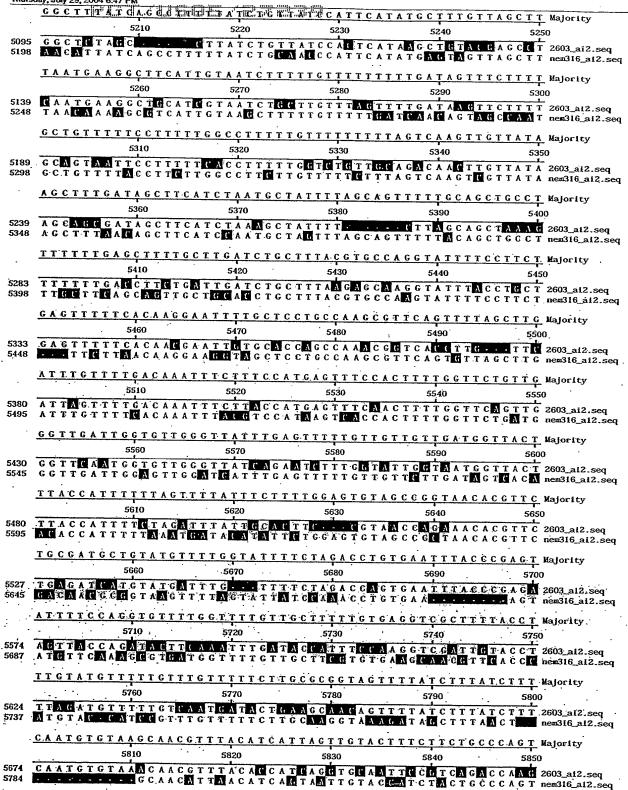
AGGTGTACATGTTAGCAAAGTCGCATAATCCTTACCTTTAACAACCAATA 2603_a12.seq

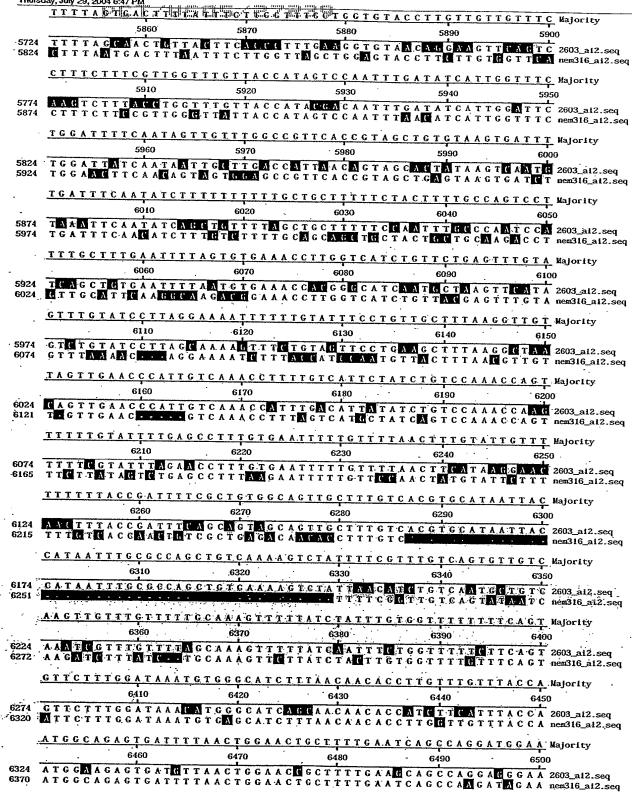
AGGTGTACATGTTAGCAAAGTCGCATAATCCTTACCTTTAACAAACCAATA nem316_a12.seq

			_	001		
• • •				93/4	87	
Thu	rment Report owo rsday, July 29, 2004 o	2006/078318	ein method with Weighted	residue weight table.		PCT/US2005
	ATTTACK	AAAATTA	Creecutta	CARCACTTAT	TTGATCAACCTT	ATAG Majority
315	1 477710	3260	3270	3280	3290	3300
325			CTGGCTTTA	C	TTGATCAACCTT TTGATCAACCTT	A T A G 2603_a12.seq
	GCTAAAA				TTTTTCCTTTTT	
220	0'0"	3310	3320	3330	3340	3350
320 330	I GCTAAAA I GCTAAAA	CTTCTTTG	A T A T T A T G A A A T A T T A T G A	A T A T A A A A A A T A T A A A A A A	TTTTTCCTTTTT	T A A G 2603_ai2.seq
	TTTATCT	AAATCTGT			AAGCCGCGATGA	TAAG nem316_a12.seq
		3360	3370	3380	3390	3400
325 335	TTTATCT TTTATCT	AAATCTGT	A A A T A A C T T A	G C T T T A G G T .	A A G C C G C G A T G A A A G C C G C G A T G A	
	TGATAAC	AGTATGTG			CAAGGAGGTTCC	-
		3410	3420	3430	3440	.3450
3301 3401	TGATAAC	AGTATGTG	AACTTTTTCC	ACCAATTGG	CAAGGAGGTTCC	
	AGGTGTC	CTGCTCCT	TTTTC		CAAGGAGGTTCC CAA <mark>A</mark> GA <mark>A</mark> GTTCC	TTC A nem316_ai2.seq
		3460	3470	3480	3490	
3351 3451	A G G T G T C	C T G C T C C T C T G C T C C T	T T T T C A A G A A	CACTACTGGT	TAGECCCCAT	3500 A G A T 2603 a12.seg
			LIIICKKGKA	CACIACIGG	L A G T C C C C C C A T .	A G A T nemi316_a12.seq
		3510	3520	3530	TATCCAATCATT1	
3401 3501	AGGTAAT		GATAGACGGT	ATATCAATAT	3540 FATCCAATCATT	3550 F C A G 2603_at2.seq.
	AGGTAAT	-	G A T.A G A C G G T	ATATCAATAT	T A T C C A A T C A T T 1	CAG nem316_a12.seq
	TARICIEA	3560			TTTTTTTCTTT	TCA Majority
3451	GAATCTC	AAGCATGT	3570 G G C C T A T T C	3580 A G C A A T A C C T	3590	3600
3551		THE TAXABLE	GGCGIAIIC	A G.C A A T A C C T	TTTTTTTCTTT	TCA nem316_a12.seq
	· ·	3610	GGCGGCTTC		TCTATTATAAGC	TTT Majority
3501	G.T A T A G G G	ATCTGAT	3620	GGTCCAGTGT	3640 TCTATTATAAGC	3650
3601				GGICCRGIGI	ICIATTATAAGC	TTT 2603_a12.seq TTT nem316_a12.seq
	TGCTAACT	3660		TCTTTAGTAT	TTAATTTTTGGG	TTT Majority
3551	TGCTAACT	CAAATCGT	3670 C T A T T A A T C	3680 .	3690 T T A A T T T T T G G G	3700
3651			CLALLARIC	ICITIA.GENAT	LIAATTTTTGGG	TTT nem316_ai2.seq
•	GATTATCA	AAGTTAGT	TACTTGATT	ATTAGCTTTA	ATATTATAGTAC	C A A Majority
3601		3/10	3720	: 3730	3740	3750
3701		11,5 -	, and the state of	diraccity.	ATATTATAGTAC ATATTATAGTAC	C A A nem316_a12.seq
	TTTGAAAT	AAAAGGAT	ATGAGGTTA	T C A A A G A C C	AACTAAGAACAA	TAG Majority
3651		3760	3770	3780	3790	3800
3751	TTTGAAAT	AAAAGGAT	ATGAGGTTA:	T C A A A A G A C C T C A A A A G A C C	A A C T A A G A A C A A A A C T A A G A A C A A	T A G 2603_a12.seq
٠,	TATCAGGC	CTACATTC	ATCCATCGAT	TTAAAACGA	CCGATTTCTTAA	C.C.T. Moderate
		3810	3820	3830	3840	3850
3701 [.] 3801	TATCAM GC TATCAGGC	CTACATTC CTACATTC	A T C C A T C G A T	TTAAAACGA	C C G A T T T C T T A A C C G A T T T C T T A A	·
	TTTTCTGA	AATTTTCC	TCCCATTATG	ATTCAATTC	CTTTTCTAACAC	TTC Water
97		3000	3870	3880	3890	2000
3751 3851	TTTTCTGA	A	T C C C A T T A T G T C C C A T T A T G	ATTCAATTC ATTCAATTC	CTTTTCTAACAC CTTTTCTAACAC	TTC 2603_ai2.seq

	CTAAAO GATT, TT	Halle Part Hall to any trape and	9 000 100	·	
	CIAAA [D'G] A, T T T T	THE GARGET EGA O	G T T T A T T A A C	CAAAGTAACCA	A G C A Majority
	3910	3920	3930	3940	3950
3801	CTAAACGATTTTT CTAAACGATTTTT	TTGACGTTGAC	CTTTTATTAAC		
3901	CTAAACGATTTT	TTGACGTTGAC			AGCA 2603_al2.seq AGCA nem316_al2.seq
	• • • • • • • • • • • •				
	ATAATAACTAAAG	ATATATAGAAT	AGATATCTATA	AATCGTGTTTA	AAT G Majority
	3960	. 3970	3980	3990	4000
3851		ATATATAGAAT	CATATOTATA		
3951	ATAATAACTAAAG	ATATATAGAAA	A G A T A T C T A T A	AATCGIGITTA	A A T G 2603_a12_seq
	ACCTTCTTTATT	AATTTTTCATCA	LATAGGACCTT	TATAAGGGATA	C G A T Majority
	4010	4020	4030	4040	4050
3901	ACCETCTTTATT	AATTTTTCATC	ATACCACCTT	T 1 T 1 1 C C C 1 T 1	
4001	ACCTTCTTTATT	AATTTTTCATCA	ATAMGACCTT	TATAAGGGATA	C G A T 2603_a12.seq
	CTCCCCTTACTAA	AAGTCTGTGTGT	TATTGATCATA	ATCGGGGTGCA	AGTT Majority
•	4060	4070	4080	4090	4100
3951	GTCCCCTTACTAA	AAGTETETET	TATTGATCATA	ATCCCCCTCC	4.0.7
4051	GTCCCCTTACTAA	AAGTCTGTGTGT		ATCGGGGTGCA	A G T T 2603_ai2.seq
	AATAAGGTTGCAT	AATCATGTCCAG	GAACAACCAA	CAAATCTGAAA	A G T T Majority
	4110	4120	4130	4140	4150
4001	AATAAGGTTGCAT	AATCATGTCCAC	GAACAACCAA	C 4 4 7 2 7 2 1 4 1	
4101	AATAAGGTTGCAT	AATCATGTCCAG	G A A C A A C C A A	C	A C T T 2603_a12.seq
-	ATCGGGTGTAACG	ACTTTTATCTGA	TCTACTTCAT	ATGCTATCGTT	TCTT Majority
	, 4160	4170	4180	4190	4200
4051	ATCGGGTGTAACG	ACTITIATETGA	TCTACTTCAT	ATCCTATCCTT	
4151	ATCGGGGTGTAACG	ACTTTTATCTGA	TGTACTTGAT	ATGCTATCGTT	TCTT nem316 at2 sec
	TTATGTTTTGAAT	ATAAAACTTATC	TCCTTTTTTT	AACTTTTTAAG	G T T A Majority
	4210	. 4220	4230	4240	. 4250
4101	TTATGTTTTGAAT	ATAAAACTTATC	TCCTTTTTT	AACTTTTAAC	0 m m 1 inner
4201	TTATGTTTGAAT	ATAAACTTATC	TCCTTTTTT	AACTTTTTAAG	GTTA nem316 at2 sea
	GAAAAGAGTTCTT		CTGAGTGCGC	TGTTATAACGG	<u>FATG</u> Majority
	4260	4270	4280	4290	4300
4151					
4000	GAAAAGAGTTCTT	TATCTGGAATTC	CTGAATGCGC	TGTTATAACAG	T A T G 2603 at2 sea
4251	GAAAAGAGTTCTT GAAAAGAGTTCTT	TATCTGGAATTC TATCTGGAATTC	CTGAATGCGC CTGAGTGCGC	T G T T A T A A C A G . T G T T A T A A C G G .	TATG 2603_ai2.seq TATG nem316_ai2.seq
4251		TRICIGGRATIC	Cieveice.	TGTTATAACGG	TATC nem316_a12.seq
4251	TGTGCTATTTCCT	C C A A T T G G A A G A	GAGGTACCTT	TGTTATAACGG	TATC nem316_a12.seq
	TGTGCTATTTCCT	C C A A T T G C A A G A 4320.	GAGGTACCTT	T G T T A T A A C G G C T A A A T G C C C T (4340	TATC nem316_ai2.seq GCTC Majority 4350
4201	TGTGCTATTTCCT	C C A A T T G G A A G A 4320.	GAGGTACCTT	T G T T A T A A C G G C T A A A T G C C C T (TATC nem316_a12.seq GCTC Majority 4350
	TGTGCTATTTCCT	C C A A T T G G A A G A 4320.	GAGGTACCTT	T G T T A T A A C G G C T A A A T G C C C T (TATC nem316_a12.seq GCTC Majority 4350
4201	TGTGCTATTTCCT 4310 TGTACTATTTCCT TGTGCTATTTCCT	C C A A T T G G A A G A 4320. C C A A T T G G A A G A C C A A T T G G A A G A	GAGGTACCTT 4330 GAGGTACCTT GAACCTTC	T G T T A T A A C G G C T A A A T G C C C T (4340 C T A A A T G C C C T (C T A A A T G C C C T (G C T C Majority 4350 G C T C 2603_a12.seq G C T C nem316_a12.seq
4201	TGTGCTATTTCCT 4310 TGTACTATTTCCT TGTGCTATTTCCT CTTTAGATAGAAC	C C A A T T G G A A G A 4320 C C A A T T G G A A G A C C A A T T G G A A G A T T C T T G A C T T G A	GAGGTACCTTC 4330 GAGGTACCTTC GANGTACCTTC	T G T T A T A A C G G C T A A A T G C C C T 6 4340 C T A A A T G C C C T 6 C T A A A T G C C C T 6	G C T C Majority 4350 G C T C 2603_a12.seq G C T C nem316_a12.seq
4201 4301	TGTGCTATTTCCT4310 TGTACTATTGCCTTGTGCTATTTCCT	C C A A T T G G A A G A 4320 C C A A T T G G A A G A C C A A T T G G A A G A T T C T T G A C T T G A 4370	G A G G T A C C T T G 4330 G A G G T A C C T T G A C C T G C A A A T A 4380	T G T T A T A A C G G C T A A A T G C C C T 6 4340 C T A A A T G C C C T 6 T A A A T G C C C T 6 A T A G G G A G T T T 7 4390	G C T C Majority 4350 G C T C 2603_ai2.seq G C T C nem316_ai2.seq C T C A Majority
4201 4301 4251	TGTGCTATTTCCT 4310 TGTACTATTGCCT TGTGCTATTTCCT CTTTAGATAGAAC 4360 CTTTAGATAGAAC	C C A A T T G G A A G A 4320 C C A A T T G G A A G A C C A A T T G G A A G A T T C T T G A C T T G A 4370	4330 GAGGTACCTT GANGTACCTT GANGTACCTT ACCTGCAAAT 4380	T G T T A T A A C G G C T A A A T G C C C T G 4340 C T A A A T G C C C T G C T A A A T G C C C T G	G C T C Majority 4350 G C T C 2603_a12.seq G C T C nem316_a12.seq C T C nem316_a12.seq T T C A Majority 4400
4201 4301	TGTGCTATTTCCT 4310 TGTACTATTGCCT TGTGCTATTTCCT CTTTAGATAGAAC 4360 CTTTAGATAGAAC	C C A A T T G G A A G A 4320 C C A A T T G G A A G A C C A A T T G G A A G A T T C T T G A C T T G A 4370	4330 GAGGTACCTT GANGTACCTT GANGTACCTT ACCTGCAAAT 4380	T G T T A T A A C G G C T A A A T G C C C T G 4340 C T A A A T G C C C T G C T A A A T G C C C T G	G C T C Majority 4350 G C T C 2603_a12.seq G C T C nem316_a12.seq C T C nem316_a12.seq T T C A Majority 4400
4201 4301 4251	TGTGCTATTTCCT 4310 TGTACTATTTCCT TGTGCTATTTCCT CTTTAGATAGAAC 4360 CTTTAGATAGAAC CTTTAGATAGAAC	C C A A T T G G A A G A 4320 C C A A T T G G A A G A C C A A T T G G A A G A T T C T T G A C T T G A 4370 T T C T T G A C T T G A T T C T T G A C T T G A	G A G G T A C C T T G 4330 G A G G T A C C T T G G A A G T A C C T T G A C C T G C A A A T A 4380 A C C T G C A A A T A A C C T G C A A A T A	T G T T A T A A C G G C T A A A T G C C C T G 4340 C T A A A T G C C C T G C T A A A T G C C C T G A T A G G G A G T T T T 4390 A T A G G G A G T T T T	T A T G nem316_a12.seq G C T C Majority 4350 G C T C 2603_a12.seq G C T C nem316_a12.seq T T G A Majority 4400 T T G A 2603_a12.seq T T G A nem316_a12.seq
4201 4301 4251	TGTGCTATTTCCT 4310 TGTACTATTTGCCC TGTGCTATTTCCT CTTTAGATAGAAC CTTTAGATAGAAC CTTTAGATAGAAC CTTTAGATAGAAC CCTATCTTAGGAAC	C C A A T T G G A A G A 4320. C C A A T T G G A A G A C C A A T T G G A A G A T T C T T G A C T T G A 4370 T T C T T G A C T T G A T T C T T G A C T T G A C T G A A A T T G T T G A	G A G G T A C C T T G 4330 G A G G T A C C T T G A C C T G C A A A T A 4380 A C C T G C A A A T A A C C T G C A A A T A C C T G C A A A T A	4340 C T A A A T G C C C T 6 4340 C T A A A T G C C C T 6 C T A A A T G C C C T 6 A T A G G G A G T T T 7 A T A G G G A G T T T 7	T A T G nem316_a12.seq G C T C Majority 4350 G C T C 2603_a12.seq G C T C nem316_a12.seq T T G A Majority 4400 T T G A 2603_a12.seq T T G A nem316_a12.seq
4201 4301 4251 4351	TGTGCTATTTCCT 4310 TGTACTATTTGCCC TGTGCTATTTCCT CTTTAGATAGAAC 4360 CTTTAGATAGAAC CTTTAGATAGAAC CTTTAGATAGAAC CTTTAGATAGAAC	C C A A T T G G A A G A 4320. C C A A T T G G A A G A C C A A T T G G A A G A T T C T T G A C T T G A 4370 T T C T T G A C T T G A T T C T T G A C T T G A C T T G A C T T G A C T T G A C T T G A C T T G A C T T G A	4330 GAGGTACCTT 4330 GAGGTACCTT GAMGTACCTT ACCTGCAAAT 4380 ACCTGCAAAT ACCTGCAAAT ACCTGCAAAT ACCTGCAAAT ACCTGCAAAT ACCTGCAAAT AA30	T G T T A T A A C G G C T A A A T G C C C T G 4340 C T A A A T G C C C T G C T A A A T G C C C T G A T A G G G A G T T T T 4390 A T A G G G A G T T T T 4440	T A T G nem316_a12.seq G C T C Majority 4350 G C T C 2603_a12.seq G C T C nem316_a12.seq T T G A Majority 4400 T T G A 2603_a12.seq T T G A nem316_a12.seq C A T Majority 4450
4201 4301 4251 4351	TGTGCTATTTCCT 4310 TGTACTATTTCCT TGTGCTATTTCCT CTTTAGATAGAAC 4360 CTTTAGATAGAAC CTTTAGATAGAAC CCTATCTTAGGAAC 4410 CCTATCTTAGGAAA	C C A A T T G G A A G A 4320 C C A A T T G G A A G A C C A A T T G G A A G A T T C T T G A C T T G A 4370 T T C T T G A C T T G A T T C T T G A C T T G A C T G A A A T T G T T G 4420 C T G A A A T T G T T G	GAGGTACCTT 4330 GAGGTACCTT GAMGTACCTT GAMGTACCTT 4380 ACCTGCAAAT ACCTGCAAAT CGATTTTTTCA 4330	T G T T A T A A C G G C T A A A T G C C C T G 4340 C T A A A T G C C C T G A T A G G G A G T T T T 4390 A T A G G G A G T T T T A C T T A C C T C T A A	G C T C Majority 4350 G C T C 2603_a12.seq G C T C nem316_a12.seq T T G A Majority 4400 T T G A 2603_a12.seq T T G A nem316_a12.seq T T G A Majority
4201 4301 4251 4351	TGTGCTATTTCCT 4310 TGTACTATTTGCCC TGTGCTATTTCCT CTTTAGATAGAAC CTTTAGATAGAAC CTTTAGATAGAAC CTTTAGATAGAAC CCTATCTTAGGAAC	C C A A T T G G A A G A 4320 C C A A T T G G A A G A C C A A T T G G A A G A T T C T T G A C T T G A 4370 T T C T T G A C T T G A T T C T T G A C T T G A C T G A A A T T G T T G 4420 C T G A A A T T G T T G	GAGGTACCTT 4330 GAGGTACCTT GAMGTACCTT GAMGTACCTT 4380 ACCTGCAAAT ACCTGCAAAT CGATTTTTTCA 4330	T G T T A T A A C G G C T A A A T G C C C T G 4340 C T A A A T G C C C T G A T A G G G A G T T T T 4390 A T A G G G A G T T T T A C T T A C C T C T A A	G C T C Majority 4350 G C T C 2603_a12.seq G C T C nem316_a12.seq T T G A Majority 4400 T T G A 2603_a12.seq T T G A nem316_a12.seq T T G A Majority
4201 4301 4251 4351 4301 4401	TGTGCTATTTCCT 4310 TGTACTATTTCCT TGTGCTATTTCCT CTTTAGATAGAAC 4360 CTTTAGATAGAAC CTTTAGATAGAAC CTTTAGATAGAAC CTTTAGATAGAAC CCTATCTTAGGAAC CCTATCTTAGGAAC CCTATCTTAGGAAC	C C A A T T G G A A G A 4320 C C A A T T G G A A G A C C A A T T G G A A G A T T C T T G A C T T G A 4370 T T C T T G A C T T G A T T C T T G A C T T G A C T G A A A T T G T T G 4420 C T G A A A T T G T T C C T G A A A T T G T T C	G A G G T A C C T T C 4330 G A G G T A C C T T C A C C T G C A A A T A 4380 A C C T G C A A A T A A C C T G C A A A T A C C T G C A A A T A C G A T T T T T T C A C G A T T T T T T C A	4340 C T A A A T G C C C T G 4340 C T A A A T G C C C T G A T A G G G A G T T T T 4390 A T A G G G A G T T T T 4440 C T T A C C T C T A A C T T A C C T C T A A	TAT G nem316_a12.seq GCTC Majority 4350 GCTC 2603_a12.seq GCTC nem316_a12.seq TTGA Majority 4400 TTGA 2603_a12.seq TTGA 2603_a12.seq TTGA T Majority 4450 CCAT Majority 4450 CCAT 2603_a12.seq TCAT mem316_a12.seq
4201 4301 4251 4351 4301 4401	TGTGCTATTTCCT 4310 TGTACTATTTCCT TGTGCTATTTCCT CTTTAGATAGAAC 4360 CTTTAGATAGAAC CTTTAGATAGAAC CCTATCTTAGGAAC 4410 CCTATCTTAGGAAA CCTATCTTAGGAAA	C C A A T T G G A A G A 4320. C C A A T T G G A A G A C C A A T T G G A A G A T T C T T G A C T T G A 4370 T T C T T G A C T T G A T T C T T G A C T T G A C T G A A A T T G T T G C T G A A A T T G T T C C T G A A A T T G T T C C T G A A A T T G T T C C T G A A A T T G T T C C T G A A A T T G T T C C T G A A A T T G T T C C T G A A A T T G T T C C T G A A A T T G T T C C T G A A A T T G T T C C T G A A A T T G T T C C T G A A A T T G T T C C T G A A A T T G T T C C T G A A A T T G T T C C T G A A A T T G T T C C T G A A A T T G T T C C T G A A A T T G T T C C T G A A A T T G T T C C T G A A A T T G T T C C T C C C C C C C T T T	GAGGTACCTT 4330 GAGGTACCTT GAMGTACCTT GAMGTACCTT 4380 ACCTGCAAAT ACCTGCAAAT ACCTGCAAAT 4330 CGATTTTTTCA CGATTTTTTCA CGATTTTTTCA	T G T T A T A A C G G C T A A A T G C C C T G 4340 C T A A A T G C C C T G C T A A A T G C C C T G A T A G G G A G T T T T 4390 A T A G G G A G T T T T 4440 A C T T A C C T C T A A C T T A C C T C T A A C T T A C C T C T A A C T T A C C T C T A A C T T A C C T C T A A	TAT G nem316_a12.seq GCTC Majority 4350 GCTC 2603_a12.seq GCTC nem316_a12.seq TTGA Majority 4400 TTGA 2603_a12.seq TTGA 2603_a12.seq TTGA T Majority 4450 CCAT Majority 4450 CCAT 2603_a12.seq TCAT mem316_a12.seq
4201 4301 4251 4351 4361 4401	TGTGCTATTTCCT 4310 TGTACTATTTCCT TGTGCTATTTCCT CTTTAGATAGAAC 4360 CTTTAGATAGAAC CTTTAGATAGAAC 410 CCTATCTTAGGAA CCTATCTTAGGAA CCTATCTTAGGAA ACGGGCGTACTCT 4460	C C A A T T G G A A G A 4320 C C C A A T T G G A A G A C C A A T T G G A A G A T T C T T G A C T T G A 4370 T T C T T G A C T T G A T T C T T G A C T T G A C T G A A A T T G T T G C T G A A A T T G T T G C T G A A A T T G T T G C T G A A A T T G T T G C T G A A A T T G T T T G C T G A A A T T G T T T G C T G A A A T T G T T T G C T G A A A T T G T T T G C T G A A A T T G T T T G C T G A C C C C C T T T 4470	4330 GAGGTACCTT 4330 GAGGTACCTT GAMGTACCTT 4380 ACCTGCAAAT ACCTGCAAAT ACCTGCAAAT CGATTTTTTCA 4430 CGATTTTTTCA TGAATTCGTTT	T G T T A T A A C G G C T A A A T G C C C T G 4340 C T A A A T G C C C T G A T A G G G A G T T T T 4390 A T A G G G A G T T T T A T A G G G A G T T T T 4440 A C T T A C C T C T A A C T T A C C T C T A A C T T A C C T C T A A C T T T C T C A T A A G 4490	TATG nem316_a12.seq GCTC Majority 4350 GCTC 2603_a12.seq GCTC nem316_a12.seq TTGA Majority 4400 TTGA 2603_a12.seq TTGA nem316_a12.seq CAT Majority 4450 CCAT 2603_a12.seq CAT mem316_a12.seq CAT Majority 4450 CCAT 2603_a12.seq CAT Majority
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4201 4301 4251 4351 4361 4401	TGTGCTATTTCCT 4310 TGTACTATTTCCT CTTTAGATAGAAC 4360 CTTTAGATAGAAC CTTTAGATAGAAC CCTATCTTAGGAAC 4410 CCTATCTTAGGAA CCTATCTTAGGAA ACGGGCGTACTCT ACGGGCGTACTCT ACGGGCGTACTCT CTTCAAGATGGAC	C C A A T T G G A A G A 4320. C C A A T T G G A A G A C C A A T T G G A A G A T T C T T G A C T T G A 4370 T T C T T G A C T T G A T T C T T G A C T T G A C T G A A A T T G T T G 4420 C T G A A A T T G T T G C T G A A A T T G T T G C T G A A A T T G T T G G C T A C C C C C T T T 4470 G C T A C C C C C C T T T G C T A C C C C C C T T T A T T A T T T A A A G A	GAGTACCTT 4330 GAGGTACCTT GANGTACCTT GANGTACCTT ACCTGCAAAT 4380 ACCTGCAAAT ACCTGCAAAT ACCTGCAAAT 4480 CGATTTTTTCA 4480 TGAATTCGTT TGAATTCGTT ATCATTATAAG	T G T T A T A A C G G C T A A A T G C C C T G 4340 C T A A A T G C C C T G C T A A A T G C C C T G A T A G G G A G T T T T 4390 A T A G G G A G T T T T 4440 A C T T A C C T C T A A G C T T A C C T C T A A G 4490 C T T T C T C A T A A G C T T T C T C A T A A G C T T T C T C A T A A G C T T T C T C A T A A G C C T T G T G C T A G A	TATG nem316_a12.seq GCTC Majority 4350 GCTC 2603_a12.seq GCTC nem316_a12.seq TTGA Majority 4400 TTGA 2603_a12.seq TTGA nem316_a12.seq CAT Majority 4450 CAT 2603_a12.seq CAT Majority 4500 CAT Majority
4201 4301 4251 4351 4301 4401 4351 4451	TGTGCTATTTCCT 4310 TGTACTATTTCCT TGTGCTATTTCCT CTTTAGATAGAAC 4360 CTTTAGATAGAAC CCTATCTTAGGAAC CCTATCTTAGGAAC A410 CCTATCTTAGGAAC CCTATCTTAGGAAC ACGGGCGTACTCT ACGGGCGTACTCT ACGGGCGTACTCT CTTCAAGATGGACA 4510	CCAATTGGAAGA 4320 CCAATTGGAAGA CCAATTGGAAGA CCAATTGGAAGA TTCTTGACTTGA	4330 GAGGTACCTT 4330 GAGGTACCTT GAMGTACCTT ACCTGCAAAT 4380 ACCTGCAAAT ACCTGCAAAT 4430 CGATTTTTTCA 4430 CGATTTTTTCA TGAATTCGTTT TGAATTCGTTT ATCATTATAAG 4530	4340 CTAAATGCCCT 4340 CTAAATGCCCT CTAAATGCCCT CTAAATGCCCT ATAGGGAGTTT 4390 ATAGGGAGTTT ATAGGGAGTTT 4440 ACTTACCTCTAA ATTCTCATAAG 4490 CTTTCTCATAAG CTTTCTCATAAG CTTTCTCATAAG 4540	TAT G nem316_a12.seq GCTC Majority 4350 GCTC 2603_a12.seq GCTC nem316_a12.seq GTGA Majority 4400 TTGA 2603_a12.seq TTGA nem316_a12.seq CAT Majority 4450 CCAT Majority 4500 CCAT Majority 4500 CCAT mem316_a12.seq CCAT mem316_a12.seq CCAT Majority 4500 CCAT Majority
4201 4301 4251 4351 4361 4401	TGTGCTATTTCCT 4310 TGTACTATTTCCT TGTGCTATTTCCT CTTTAGATAGAAC 4360 CTTTAGATAGAAC CTTTAGATAGAAC CCTATCTTAGGAAC 4410 CCTATCTTAGGAAC CCTATCTTAGGAAC CCTATCTTAGGAAC 4460 ACGGGCGTACTCTC ACGGGCGTACTCTC CTTCAAGATGGACA 4510 CTTCAAGATGGACA	C C A A T T G G A A G A 4320 C C A A T T G G A A G A C C A A T T G G A A G A T T C T T G A C T T G A 4370 T T C T T G A C T T G A T T C T T G A C T T G A C T G A A A T T G T T G 4420 C T G A A A T T G T T C C T G A A A T T G T T C C T G A A A T T G T T T 4470 G C T A C C C C C T T T G C T A C C C C C T T T G C T A C C C C C T T T A T T A T T T A A A G A 4520	GAGGTACCTT 4330 GAGGTACCTT GAMGTACCTT GAMGTACCTT ACCTGCAAAT 4380 ACCTGCAAAT ACCTGCAAAT 4430 CGATTTTTTCA 4430 CGATTTTTTCA TGAATTCGTT 4480 TGAATTCGTT ATCATTATAAG 4530 ATCATTATAAAG	4340 CTAAATGCCTT 4340 CTAAATGCCCT CTAAATGCCCT ATAGGGAGTTT 4390 ATAGGGAGTTT ATTTCTCATAAG ATTTCTCATAAGAG ATTTCTCATAAGAG ATTTCTCATAAGAGAAGAG	TATG nem316_a12.seq GCTC Majority 4350 GCTC 2603_a12.seq GCTC nem316_a12.seq TTGA Majority 4400 TTGA 2603_a12.seq TTGA nem316_a12.seq CAT Majority 4450 CAT 2603_a12.seq CAT Majority 4500 GAT Majority 4500 GAT 2603_a12.seq GAT Majority 4500 GAT 2603_a12.seq GAT Majority 4500 GAT 2603_a12.seq GAT Majority
4201 4301 4251 4351 4361 4401	TGTGCTATTTCCT 4310 TGTACTATTTCCT CTTTAGATAGAAC 4360 CTTTAGATAGAAC CTTTAGATAGAAC CCTATCTTAGGAAC 4410 CCTATCTTAGGAA CCTATCTTAGGAA ACGGGCGTACTCT ACGGGCGTACTCT ACGGGCGTACTCT CTTCAAGATGGAC	C C A A T T G G A A G A 4320 C C A A T T G G A A G A C C A A T T G G A A G A T T C T T G A C T T G A 4370 T T C T T G A C T T G A T T C T T G A C T T G A C T G A A A T T G T T G 4420 C T G A A A T T G T T C C T G A A A T T G T T C C T G A A A T T G T T T 4470 G C T A C C C C C T T T G C T A C C C C C T T T G C T A C C C C C T T T A T T A T T T A A A G A 4520	GAGGTACCTT 4330 GAGGTACCTT GAMGTACCTT GAMGTACCTT ACCTGCAAAT 4380 ACCTGCAAAT ACCTGCAAAT 4430 CGATTTTTTCA 4430 CGATTTTTTCA TGAATTCGTT 4480 TGAATTCGTT ATCATTATAAG 4530 ATCATTATAAAG	4340 CTAAATGCCTT 4340 CTAAATGCCCT CTAAATGCCCT ATAGGGAGTTT 4390 ATAGGGAGTTT ATTTCTCATAAG ATTTCTCATAAGAG ATTTCTCATAAGAG ATTTCTCATAAGAGAAGAG	TATG nem316_a12.seq GCTC Majority 4350 GCTC 2603_a12.seq GCTC nem316_a12.seq TTGA Majority 4400 TTGA 2603_a12.seq TTGA nem316_a12.seq CAT Majority 4450 CAT 2603_a12.seq CAT Majority 4500 GAT Majority 4500 GAT 2603_a12.seq GAT Majority 4500 GAT 2603_a12.seq GAT Majority 4500 GAT 2603_a12.seq GAT Majority

AE			•	95/487		PCT/US200
Thurs	nent Report of AVV U Z day, July 29, 2004 6:47 P	Milia in the Hall of the Market	od with Weighted residue w	reight table.	•	PC 17US200
		•	TT OT CAETAA		AGCTCTCTCA	A A Kajority
4451		4560 T T C A T T T C 1	4570 F.T.T.C.T.C.A.C.T.A.A	4580	A S C T C T C T C A	4600
4551	ATACGNCGA	TTGATTTCT	TTTCTGACTAA		C A G C T C T C T C A C A G C T C T C T C A	A A 2603_a12.seq A A nem316_a12.seq
	ATCCTGTGT	TTGATTATT 4610		•	AACGTGATAC	•
4501	ATCCTGTGT	TTGATTATT	AGATTCTATO	4630 G T A T A G T A A A	AACGTGATAC	4650 C A 2603_ai2.seg
4601		IIGALIALI	IAGATTCTATO	GTATAGTAAA	AACGTGATAC	C A nem316_ai2.seq
		4660	4670	4680	A T G A T A A A G 6	GA Kajority 4700
4551 4651	CTGGATACA CTGGATACA	. A T A A A A T A G	ATÁGACCTAT ATÁGACCTAT	TAGAAAAAGA	ATGATAAAAG	G A 2603_a12.seq
					TTTTTTAGTC	
		1710	-4720	4730	4740	4750
4601 4701	A G A T T T G A C	T T C T T C T T T	TTTTTTGTTT TTAGTTT	TTTTGATGAT TTTTGTTGAT	TTTTTTAGTC	T T 2603_ai2.seq T T nem316_ai2.seq
			•		AAGAGTACTT	
ACE 1		760	4770	4780	4790	4800
4031 4748	CACGTCATC	TCCTAGATA	ATGGCTCTTG ATGGCTCTTG	C T T A T G A T C T	AAGAGTACTT	CT 2603_ai2.seq CT nem316_ai2.seq
			-	GCTTTAACTG	TGCTTATACA	<u>r C</u> Kajority
4701		CCCTTAGAT	4820 CATAACCA	4830	4840 GCTTATACA	4850
4798	ACIGARATA	CCCITAGAT	CATAAGCACA	GCTTTAACTG	T-G C T T A T A C A	C nem316_ai2.seq
		TAGCCTTAA 860.	· ·		TTTCATGATAA	A C Majority .
4751	ATCAAAGAC	TAGCCTTAA	GCTTCCTTTG	4880 A T T C C C T C T	TTTCATCATA	4900
4848	A I CAAAGAC	INGCCIIAA	CCTTCCTMTG	ATTOMCGTTT	TTTCATGATAA	A C. nem316_ai2.seq
		<u> </u>	GCTTAAACCA 4920	A T A A T T G T G A 4930	AAAGAATTGTA	•
1801 1898	TACTGCTCC	AAGCATAAT	GCTTAAACCA	ATAATTCTCA	AAACAATTCTA	4950
1090		AAGCATAAT	GCTTAAACCA	ATAATTGTGA	AAAGAATTGTA	A C nem316_ai2.seq
		960	4970	4980	T G T A C T T G T T T	G Majority 5000
1851 1948	CAATACCAC CAATACCAC	CTGTTTGTG CTGTTTGTG	G G A T T G T T A C	CTTTTTATTT	T C T A C A C G T G T T G A A C T T G T T G	2000 10
					A G T T T A G C C C	
		010	5020	5030	5040	5050
1901 1998	G C A T C T T T T G C A T C T T T T	TTTACAGAT	TTGCTGTTAG	GAACGTAGTC ATGCGATGTC	AATGITACCAC AGTTGIAGCCC	C 2603_ai2.seq
					TACCTGCCAAT	· •
		060	5070			5100
1945 1048	THETATETA	T G A C C C T T G T G A T G T G G C	ATTAACTACA AGTTACTTCA	A	TACCTGCCAAC CACCTGACAAT	T 2603_a12.seq
		•			TAAGTGCCTTT	
995		CTCCTCCAC	5120	5130	5140 S TAAGTACCIT	5150
098	TCGCATANC	CTGCTGGTG	CTTGAGTTTC	T T C C A A G C T A	TAAGTACCUTU TAAGTGCCTTT	T 2603_a12.seq N nem316_a12.seq
				GGTCGTTTGA	G G T G T A T T T A A	T Majority
n45	GCMA-GACCT	GTAAGTTCA	5170	5180		5200
148	TCCANACCA	GTAATTTCA:	AATTGACCTT	GATEGTTTGA GGCGTTAGA	A G T G T A L G T A A G A T C A A T T T A A	T 2603_a12.seq nem316_a12.seq





-	CCGTTCI	CIT'C'IT' TICH	I A G T T	200						
	3 3 1 1 1 1 1 1 1 1	6510	I JAMES II II II		TTT CT		TCAAC	CGATT	TTGTACT	T Majority
6374	CCURRIE			6520		6530		6540	6	550
6420	CCGTTGT	TATEG	r a a g T a r a g T T T	GATT:	TTTCT	TTA A CT TTCAAT	TCAAC	CAATT CGATT	TTAAACT TGGTAAG	2603_a12.seq T nem316_a12.seq
	TCCTTTT									
		6560		6570		6580	<u> </u>	6590		•
6424	CCTTT	AATCCT	TTGGT	GTTG	AAMC	AACTC		1 n n m	T - 100	600 <u>G</u> 2603_a12.seg
6470				G I I	CAAGC.	A A A A A C C	AGTG	rc T T T	IGTTAAC	nem316_ai2.sec
	TTGATCC	A G G C A. C	GGCCT	CATCI	TTAT	TTTCTT	TTGTI	TCCG	GAGTATC	<u>C</u> Majority
		6610		6620		6630		6640	6	650
6474 6520	CTGA	A A G A A C	GGCCT	CATCA CAUCI	ATAT	TACTE	TAGUI	TCAG	A G T A C C	2603_ai2.seq G nem316_ai2.seq
	TCTTTCT	TAATTA	AGGET	GGTGT	TAAT	ГТСТТА	сстто		CCTTAA	T Valority
		6660		6670		6680		6690		700
6524	TCTTAT	TAATTA	AGGET	GGTGT	TAATT	TTGTTA	CCTTC		CCTTAI	2603_ai2.seq
6567	ACT TECT	T A	· · · · ·				· · · C C	TTTT	CAGTAA	T nem316_a12.seq
•	GTATTGC	ATTTTA	CCAGT	TTTAT	TTTTT	TTCAA	A G C T A	AAGCA	AAGAAC	G. Vaforter
		6710	,	6720		6730		6740		750
6574	ATATTGC	ATTTA	CCATT	TTTAT	CTTCT	TTCAA	AGCTA			1.,
6590			CCKUI	I, I EN A I	T T T T		A	AAAC	AAGAAA	G nem316_at2.seq
	CACCTTT	GATTTC	TTTAG	CTTCG	TTTGA	GCCAA	AGTAA	GCTTT	AAGGTC	. Majority
	-	6760	•	6770	•	6780		6790		100
6624 6628	CACCTTC	GATTTC	TTTAG	ATICU	T (GCCAA	AGTAA	CCAGC	11 1 2 2 2 2	<u>L </u>
0020	CACCELL	MAILLE	TTTAG	CATCG	H T T G A	GCCAA	AATAA	GATTT	AAGGTC	A 2603_a12.seq A пеш316_a12.seq
	TTAATTT	GTTTAC	CTTTG	TAGTC	TTTTT	CGTTC	TTACC	TTTTG	TTCCTT	Majority
_		6810		.6820		6830		6840		50
6671 6678	GAAATAG TTAATTT	CTCCAC GTTTAC	C T T T G	T.A.G T C T A A T C	TTTTC	C G T T A	A G A C C T T A C C	т с т А с т т т т с	TTECTG TACCTT	2603_a12.seq nem316_a12.seq
	GGAGTTA									
		6860	• •	6870		6880	ONONA	6890	69	• -
6721	GAAGTTA	CTTTTG	TTAAG	ATTTE	ATTCG	GTTT	CASAA			- .
6728.			A REAL VIEW	- MINISTER G	CIIGI	Guille VI	GACAA	TCTTG	TGCAAGG	nem316_ai2.seq
	TCACTGT	ATTAGT	TGTTG	CTTCG	TCCGC	AAACG	стббт	GCAAC	TGAGAGI	Majority
		6910		6920		6930		6940	69.	50
6771 6775	TCACTGT	ATTAGT	TGTTG	CTTCA	TCCGC	AAACG	CTGGT	GCAAC	TGAGAG	2603_a12.seq
01.10	I O II OMAGO I	A TANK A .U.	I G I I I I I	CMITCG	10060	AAACG	CTGGT	GCAAC	TGAGANT	nem316_ai2.seq
	AGTGACG	TTAAGG	TCAGT	AGCAG	TGTCG	AGAAC	ATTGT	A A G A T	ATTTGTT	Majority
		6960	•	6970 .		6980		6990	700	io
6821 6825	ATGACG	TTAANG	TCAGT	A C A A	TGCCG	AGAAC	ATTG	AAAAT	ATTTGTI	2603_ai2.seg
0023		T T IL IL OFFI	CUMBEL	A G C A G	rerce.	AGAAC	AUTGT	AAGAG	ATTTGTT	nem316_a12.seq
	GATTTTT	TTCATT	CTATO	TCCT	TCTTA.	TTTTA	TTAA	TCAAC	ATGGTTA	Majority
		7010		7020		7030		7040	705	io .
6871	GATTCTT:	TTCATT	TCTAT	CTCCT	TCTTA	TTTTA	GTTAA	TCAAC	ATGATTA	2603:a12.seg
6875		·	·		ICIIA	TIMETA	GTTAA	TCAAC	A TAGATA	nem316_a12.seq
	ATAATAT	CCGATI	TAATT	ATTA	CCGCA	GEACC	CTCC	TTTCA	AGTCATG	Majority
		7060	•	7070	•	7080	:	7090	710	0
6921 6025	ATAATAT	CCCAT	TTAAT	A (A :	CCGCA	GCACCA	CTCC	TTCA	AGTCATG	2603_a12.seq
6 925	A T A A T A TEL	ge G.G A I	THEFTY	L X .L T X	CCCCA	G C A.C C /	CTCC	TTTC		nem316_a12.seq
	GAATTTTA	TTTAAT	TTAATT	AAGA	ATACT,	A:A A G C G	CATG	A T.T T T	TAATETT	Majority
•		7110	•	7120		7130		7140	715	n
5970 5967	GAATTTT	TTAAT	TAATT	AAGA	ATACT.	AAAGCC	CATA	ATTTT	TAATCTT	2603_ai2.seg
201	GAATTAT		LTAAT.1	TAAGA	ATACT.	AAANC	CATG	A T T T T T	FAATCTT	nem316 a13 acc

Thurs	day, July 29, 2004 6:47 Pt	M	one only may make made the	•		
	TTTTTCTGG	ATATATOA	CTAGATTT CT	ATATCTTTT	CCAAATATAAA	T T Majority
	7	7160	7170	7180	7190	7200
7020	TTTTGATGG	ACATATCA	CTAGATTTCT	TATACCTTTT	CCAAATATAAA	T T 2603 at 2 cag
7017	TTTMTCTMG	ATATATCA	CTAGATTTCTT	TATATCTTTT		T T nem316_a12.seq
					T G A A G A T A G A	
		210	7220	7230	•	•
7070		•			7240	7250
7067	CCACCTGCA	ATAGACAT	C A T A G AT T C C A (CTATTAAAA.	T G A A A G A T A G A F G A A A G A T A G A	A T 2603_a12.seq
			<u>r c g g a a t a a t t</u>	CCTTTTGGT	GGAATATGCGT	G.T Majority
		260	7270	7280	7290	7300
.7120` 7117	TCCTTTCCC	ACCTGTCA	TAGGAATAATI	CCTTTTGGT	GGAATATGCGT	G T. 2603_a12.seq
****	100111000	ACCIGICA	T C G G A A T A A T 1	CCTTTTGGT	GGAATATGCGT	G T nem316_a12.seq
	TGGTAATTA	AATGCTTG	CACCTTCCTC	ATGATATTCA	IGAAATCTGTT	T A Waterity
		310	7320	7330	7340	
7170	TGGTAATTA	AATGCTTG	FCACCTTCCTC		AGAATCTGTT	7350
7167	TGGTAATTA	AATGCTTG	CACCTTCCTC	ATGATATTC	A G A A A T C T G T T	T A 2603_a12.seq T A nem316 a12 seq
•				•		_
•				•	TTCAAAAGTT	A A Majority
.2200		360	7370	7380	7390	7400
7220 7217		A T T A T A T T T	TTTATCGATC	CTTTAACCAC	TTCAAAAATT	A A 2603_a12.seq
			i i		CTTCAAAAGTT	
	AATTGGTTT	A T·T A.G T A A T	TTTTTGATAA	TCCTTCGGCG	SAAACTGCTTC	T A Majority
•		410	7420	7430	7440	7450
7270	AATTGGTTT	ATTAGTAAT	TTTTTGATAA	TCCTCCGGCG	AAACTGCTTC	T. 4 .2002 - 12 :
7267	AATTGGTTT	ATTAGTAAT	TTTTTGATAA	TCCTTCGGCC	GAAACTGCTTC	T A nem316_a12.seq
_	TTAACTGAT	ATTTGCCAT	CTTTCAAATC	TTTCT	ATTTTGCCGT	ு இரும்பார். இது இந்த நடி
		160	7470	7480	7490	
7320	TTAACTGAT	ATTTCCCA			ATTTTGCCGT	7500
7317	TTAACTGAT	ATTTGCCAT	CTTTCAAATC	TTTGTAAGAA	ATTTTGCCGT	T T 2603_ai2.seq T T nem316_ai2.seq
•	TCTCCCGTC					
•			· · · · · · · · · · · · · · · · · · ·	^	TAAATAAAGT	TT Majority
7370		10	7520	7530	7540	7550
7367	TCTCCCGTC	A CTA CTTTT A CTA CTTTT	`	TTTTTTTGG	T A A A T A A A G T	T T 2603_a12.seq
•						-
			TTGAAGTTCA	AACGTAGCTC	CTTTGAGAAG	C A Majority
	75	60 .	7570	7580	7590	7600
7420	ATAATCTTC		T·T G A A G T T C A	AACGTAGCTC	CTTTGAG'AAG'	C A 2603_a12.seq
7417	ALAKICITCA	ATTAAATTC	TTGAAGTTCA	AACGTAGCTC	CTTTGAGAAG	C A nem316_ai2.seq
	ACTTATTATT	TATCTTTAT	CAACTTTTGT	AAATTCAATT	TCACCTAACT	T C Malority
• • •		10	7620	7630	7640	7650
7470	ACTTATTAT	TATCTTTAT	CAACTTTAT		TCACCTAACT	
7467	ACTTATTATT	TATCTTTAT	CAACTTTTCT	AAATTCAATT	TCACCTAACT	T.C. nem316 at 2 seq
			ATTGTAGGAT			
						<u>FT</u> Majority
- خاند	76	15 m	7670	7680	7690	7700
7520 7517	TICICGTTTT	[T A A T C G T T	ATTGTAGGAT	ATTCTCTCAC	ATCACGAATT ATCACGAATT	T T 2603_ai2.seq
						· ·
	AGGGATTGGA	AAATCTCT	AAGTGTATTA	G G'A T C C T C T G	ATTAGGATT	C.A. Wajority
	77		7720	7730		7750
.7570	AGGGATTGGA	AAATCTCT	A.A G T'G T'A T T A	GGATCCTCTC	ATTACCATT	C 4 2002 212
7567	AGGGATTGGA	CAAATCTCT	AAGTGTATTA	GGATCCTCTG	ATTTAGGATT	C A nem316_ai2.sed
					A T A A A A C T G T (
		60	-	• •	•	
7620			7770	7780		7800
7620 7617	ATGTTGTTCT	ACCATTAG	TGTCATAGAA	T T T G T T A C T T	A T A A A A C T G T C	A 2603_a12.seq
			- J . U . L A U A A .		A L A A A A U L U T (A nemaio_ai2.seq

	TCTAGT	"T"C"A C IA ITEC	Allen Kur Garanti Alic Mic	The CTTTTC	CCTTCTCCTA	· · · · · · · · · · · · · · · · · · ·
					CCTTCTCCTA	A G T T Majority
		7810	7820	7830	7840	7850
7670 7667	T C T A G T T T C T A G T T	TCACATC	A TATGTGAGTG A TATGTGAGTG	TTACTTTTTG	CCTTCTCCTA	AATT 2603_ai2.seq AGTT nem316_ai2.seq
	CAAACCT	CTAACGT	AGAGTTTATTT	TTCATCTATTC	CTAATTTAACC	
		7860	-	• .		CCTT Majority
7720	C 1 1 1 0 0 m		7870	7880	7890	7900
7720 7717	CAAACCT	CTAACAT	A G A G T T T A T T T A G A G T T T A T T T	E E G A T G T A T T C T T G A T G T A T T C	TAATTTAACC TAATTTAACC	C C T T 2603_ai2.seq C C T T nem316_ai2.seq
	TAAGTAT	TCCACCA	TCATTATTAGG	CCCACCAGTTG	CAATGCTATC	TTTC Voluntum
		7910	7920	7930	7940	7950
7770	TAAGTAT	T C C.A C C.A	TCATTATTAGG	CCCACCAGTTC	CAATACCATC	TTC 2603 al2.seg
7767	IXXGIAI	ICCACCA	CATTATTAGG	CCCACCAGTTG	CAATGCTATC"	TTTC nem316_ai2.seq
	<u> </u>			AAGIAIAA1.CA	CTTGGTTGTA	A T G T Majority
7020	4774640	7960	7970	7980	7990	8000
7820 7817	A I I A I A C	IICCAIC	ATTICCCTGTA	AAGTATAATCA		ATGT nem316_a12.seq
	TTGTCCG	TTGCCAA	GCTGTAAATTG	A T T T T G T C A C C	CATAGGATCT	C T A Majority
		8010	8020	8030	8040	8050
7870 7867	TTGTCCA	T T A C C A A T T G C C A A	G C T G T A A A T T G G C T G T A A A T T G	A T T T T A T C A C C A T T T T G T C A C C	CATAGGATCT	T C T A nem316_a12.seq
	TAGTTCC	ATTAACA	ATTGAGTTTTC	TTTTGTTAAAA	TCTTTTCAAAT	TGT Malority
: '		8060	8070	8080	8090	8100
7920	TAGTTCC	ATTAACA	ATTGAGTTTTC	TTTTGTTAAAA	TCGTTTCAAAT	F T G T 2603 212 222
7917.	TAGTTCC	ATTAACA	ATTGAGTTTTC	TTTTGTTAAAA	CTTTTCAAA1	T C T nem316_a12.seq
	TGCTGAA	TTTTAGA	TAAAATTTCAT	TGTTAGATGTA	TCGGCTGAAGI	TAC Majority
		8110	8120	8130	8140	. 8150
7970 7967	TGCTGAA	TTTTAGA	TAAAATTTCAT	T G T T A G A T G T A	TCGGCTGAAGT	T A C 2603_ai2.seq
1301						TAC 2603_a12.seq TAC nem316_a12.seq
•	TATCGGG	GTGTAGT.	A C T C A G G T T T G (G A A G A G A A T G A	CTTCATTAGTT	CTG Majority
		8160	8170	8180	8190	8200
8020 8017	G A T A G G G · T A T C G G G	СТСТАСТ. СТАТААТ.	A C T C A G G T T T G A C T C A G G T T T	G A A G A G A A C G A G A A G A G A A T G A	CTTCATTAGTT CTTCATTAGTT	CTG 2603_ai2.seq CTG nem316_ai2.seq
	TTATTTC	TCCATCT	GAAAGTTTAAA	AGCTTCCTCTT	TCAATTTTTGA	A A. A Valority
		8210	8220	8230	8240	8250
8070	THATTC	TCCATCT		· -	TCAATTTTGA	
3067	TTATTTC	CCATCT	GAAAGTT AAAA	GCTTCCTCTT	TCAATTTTTGA	AAA 2603_ai2.seq AAA nem316_ai2.seq
	GTACCATO	CTTGATT	TTTCTTATACT (CTCATTATAA	ACTTGTCTAAA	A G C Majority
	<u></u>	8260	8270	8280	8290	8300
120 .	GTACCAT	CTTGATT	TTCTTATACT	CTCATTATAA	ACTTGTCTAAA	A C 2603 212 con
>1.1. <i>t</i>	GIACCAI	CILGATI	TTTCTTATAMT	CTCATTATAA	ACTTGTCTAAA	A G C nem316_a12.seq
	AGATATA			TGTCATAATT	TTTCTCTTTTA	AAC Najority
		8310	8320	8330	8340	8350
		·OIAIAC	A A A A I I A A A G A	LIGICALAATT		A A C nem316_a12.seq
٠.	TATTATA	TAAAGTI	TGGTTGGTGTT	CCATGTTCTT	TTACTGGTCCA	TTT Najority
		8360	8370	8380	8390	8400
220 _. 217	TATTTAT	ATAAAGTT ATAAAGTT	TGGTTGGTGTG TGGTTGGTGT1	CCATGTTCTT CCATGTTCT	TC A C T G G T C C A T T A C T G G T C C A	T T T 2603_a12.seq T T T nem316_a12.seq
	CGATAAAT	TGTACCT	TTAGGGTAATT	AAGATTTAAA	TCTAAATAATG	A A G Majority
. :		8410 .	8420 .	8430	8440	8450
270	CGATAAAT	TTGTACCT	TTAGGGTAATT	AAGATTTAAA	TCTAAATAATG	
401	UGAIAA	LIGIACCT	TTAGGGTAATT	'A A C A T T T A A A .	TCT 4 4 4 T 4 4 T C	4 4 0 000 00

Thurse	day, July 29, 2004 6:47 P		" mult make male made than			
	TTTTTCTAA	A G T THE C'C A C'A	GATTATCTCT	GTTTGATAAC	TATCTAAGGG	A A Majority
•	•	8460	8470	8480	8490	8500
8320	TTTTTGTA	AGTTTCCAGA	GATTATCTGT	GTTTCATAAC	TATCTAAGGG	•
8317	TTTTTGTA	AGTTTCCAGA	GATTATCTGT	GTTTGATAAC	TATCTAAGGG	A A nem316 a12 seg
	ACAAAAGT	TAACTCTCCC	CATTTCCTTT	TATATCCTCG	GGCTTATCAG	T A Majority
		8510	8520	8530	8540	8550
8370	ACAAAAAGT	TAACTCTCCC	CATTTCCTTT	TATATCCTCG	G G C T T.A T C A G	T A 2603 at2.seg
8367	ACAAAAAGT	TAACTCTCCC	CATTTCCTTT	TATATCCTCG	$\mathbf{G} \ \mathbf{G} \ \mathbf{C} \ \mathbf{T} \ \mathbf{T} \ \mathbf{A} \ \mathbf{T} \ \mathbf{C} \ \mathbf{A} \ \mathbf{G}$	T A nem316_ai2.seq
•	AGTACAAAA		TTT164T4T6	C 4 T T T T T T T T T T T	CATTTGTTCA	
		•	•	•		A A Majority
		8560	8570	8580	8590	8600 .
8420 8417	AGTAGAAAA	ATTACTTTTA	TTTAGATATC	CATTTTTT	CATTTGTTCA	A A 2603_ai2.seq
0417	, GIRGRAA	RIIRCIIIIR	TITAGATATO	CATTTTTTT	CATTTGTTCA	A A nem316_a12.seq
	TTGGCTTTC	CATATGATGC	ACCCAGTTTA	AAATTATTAA	TAGCATATGA	T C Majority
		8610	8620	8630	8640	8650
8470	TTGGCTTT	CATATGATGC	ACCCACTTA		TAGCATATGA	_
8467	TTGGCTTTC	CATATG.ATG.C	ACCCANTTTA	AAATTATTAA	TAGCATATGA	IC 2603_a12.seq TC nem316 a12 seq
			•	•		
	TTGTTGGAA	<u>LÇACCATÇAG</u>	TTATATGAAC	AATAATTTT	TGACTATTTC	G A Majority
	:	8660	8670	8680	8690	8700
8520	TCGTAGGAA	A.C. A C C.A T C A G	TTALATGAAC	AATAATTT	TGACTATTTC	G.A 2603 al2.seq
8517	TTGTTGGAA	ACACCATCAG	TTATATGAAC	A A T A A,T T T T T	TGACTATTTC	G A nem316_a12.seq
			TCATCTCCCT		TTTCATAGTA	
		•	•	• ,	•	7.47
		8710	8720	8730		8750
8570 8567	TTTACTTGA	ACTCAAAATA	T C A T.C T G C C.T	CCATGAAGGC	TTTCATAGTA	A A 2603_a12.seq
. 6307	IMITACIIGA	CICAAAA.IA	ICAICTECET	CCATGAAGGCC	TTTCATAGTA	A A nem316_ai2.seq
	TGTTTCTCC	TACTTACT	AAGATAGTAC	TGCTTTTGTT	G C T C T G G A G T	T A Majority
•		8760	•	•		- • • -
		0700 ,	8770	8780.	8790	XXAA
8620				8780.		· 8800
8620 8617	TGTTTCTCC	TACTTACT	AAGATAGTAC	TECTTTETT	GCTCTGGAGT	
	TGTTTCTCC TGTTTC T CC	CTACTTTACT CTACTTTACT	A A G A T A G T A C A A G A T A G T A C	T C C T T T T G T T T G C T T T T G T T	G C T C T G G A G T G C T C T G G A G T	T A 2603_a12.seq A nem316_a12.seq
	TGTTTCTCC TGTTTCCCC	TACTTACT TACTTACT	A A G A T A G T A C A A G A T A G T A C	T C C T T T T G T T T G C T T T T G T T	GCTCTGGAGT	T A 2603_a12.seq A nem316_a12.seq
	TGTTTCTCC TGTTTCTCC	TACTTTACT TACTTTACT TAGTTGATC	A A G A T A G T A C A A G A T A G T A C C C C A T T T A G C 8820	T C C T T T T C T T T G C T T T T C T T T T T A G G A G C T 8830	G C T C T G G A G T G C T C T G G A G T T C T G T C G G A A 1 8840	T A 2603_a12.seq A A nem316_a12.seq F C Majority 8850
8617	TGTTTCTCC TGTTTCCCC	TACTTTACT TACTTTACT TAGTTGATC 8810	A A G A T A G T A C A A G A T A G T A C C C C A T T T A G C 8820 C C C A C T T A G C	T C C T T T C T T T G C T T T T G T T T T T A G G A G C T 8830 T T T A G G A G C T	G C T C T G G A G T G C T C T G G A G T T C T G T C G G A A T 8840 T C T G T C G G A A	T A 2603_a12.seq A A nem316_a12.seq C Majority 8850 C C 2603_a12_seq
8617	TGTTTCTCC TGTTTCCCC	TACTTTACT TACTTTACT TAGTTGATC 8810	A A G A T A G T A C A A G A T A G T A C C C C A T T T A G C 8820 C C C A C T T A G C	T C C T T T C T T T G C T T T T G T T T T T A G G A G C T 8830 T T T A G G A G C T	G C T C T G G A G T G C T C T G G A G T T C T G T C G G A A 1 8840	T A 2603_a12.seq A A nem316_a12.seq C Majority 8850 C C 2603_a12_seq
8617	TGTTTCTCC TGTTTCCCC GTCCGTTTG ATCCATTGG GTCCGTTTG	TACTTACT TACTTACT TAGTTGATC 8810 TAGTAGATC TAGTTGATC	A A G A T A C T A C A A G A T A G T A C C C C A T T T A G C 8820 C C C A T T T A G C C C C A T T T A G C	T C C T T T T G T T T G C T T T T G T T T T T A G G A G C T 8830 T T T A G G A G C T T T A G G A G C T	G C T C T G G A G T G C T C T G G A G T T C T G T C G G A A T T C T G T C G G A A T T C T G T C T G G A A T C T G T G T A G G A A T	T A 2603_a12.seq A nem316_a12.seq F C Majority 8850 F C 2603_a12.seq F C nem316_a12.seq
8617	TGTTTCTCC TGTTTCCCC GTCCGTTTG ATCCATTGG GTCCGTTTG CTTTTTATA	TACTTTACT TACTTTACT TAGTTGATC 8810 TAGTAGATC TAGTTGATC	A A G A T A G T A C A A G A T A G T A C C C C A T T T A G C 8820 C C C A T T T A G C C C C A T T T A G C	T C C T T T T G T T T G C T T T T G T T T T T A G G A G C T 8830 T T T A G G A G C T T T A G G A G C T T T A G G A G C T	GCTCTGGAGT GCTCTGGAAT ES40 TCTGTCGGAAT CTGTCGGAAT CTGTCGGAAT	T A 2603_ai2.seq A h nem316_ai2.seq C Majority 8850 C 2603_ai2.seq C C nem316_ai2.seq T T Majority
8617 8670 8667	TGTTTCTCC TGTTTCCCC GTCCGTTTG ATCCATTCC GTCCGTTTG GTCCGTTTG	TACTTTACT TACTTTACT TACTTTACT TAGTTGATC 8810 TAGTAGATC TAGTTGATC TAGTTGATC	A A G A T A G T A C A A G A T A G T A C C C C A T T T A G C 8820 C C C A T T T A G C C C C A T T T A G C G C A T T A T T T G	T C T T T T G T T T G C T T T T G T T 8830 T T T A G G A G C T T G T A G G A G C T T T A G G A G C T T T A G G A G C T	G C T C T G G A G T G C T C T G G A G T T 8840 T C T G T C G G A A T T C T G T C G G A A T T C T G T C G G A A T T C T G T A T A A T 8890	T A 2603_a12.seq A nem316_a12.seq C Majority 8850 C 2603_a12.seq C C nem316_a12.seq T T Majority 8900
8617	TGTTTCTCC TGTTTCCCC GTCCGTTTG ATCCATTGG GTCCGTTTG CTTTTTATA CTTTTTATA	TACTTTACT TACTTTACT TAGTTGATC 8810 TAGTTGATC TAGTTGATC ATCTCTTCA 8860	A A G A T A G T A C A A G A T A G T A C C C C A T T T A G C 8820 C C C A T T T A G C C C C A T T T A G C G C A T T A T T T G 8870 G C A T T A T T T G	T C C T T T G T T T G C T T T T G T T T G T T T G T T T G T T T A G G A G C T T T T A G G A G C T T T T A G G A G C T T T A A T T G T T T T A A T T G T T T T	G C T C T G G A G T G C T C T G G A G T T S 8840 T C T G T C G G A A T C T G T C G G A A T C T G T C G G A A T C T G T A T A A T 8890 A T G A C T A T A A A T	T A 2603_a12.seq A nem316_a12.seq F C Majority 8850 F C 2603_a12.seq F C nem316_a12.seq F Majority 8900 F T 2603_a12.seq
8617 8670 8667 8720	TGTTTCTCC TGTTTCCCC GTCCGTTTG ATCCATTG GTCCGTTTG CTTTTTATA CTTTTTATA CTTTTTTATA	TACTTTACT TACTTTACT TACTTTACT BEIO TAGTTGATC TAGTTGATC TAGTTGATC TAGTTGATC ATCTCTTCA BEOO TATCTCTTCA	A A G A T A G T A C A A G A T A G T A C C C C A T T T A G C 8820 C C C C A T T T A G C C C C A T T T A G C G C A T T T A T T T G 8870 G C A T T A T T T G G C A T T A T T T G	T C C T T T T G T T T G C T T T T G T T 8830 T T T A G G A G C T T T A G G A G C T T T A A T T G T T T 8880 T T A A T T G T T T T A A T T G T T T	G C T C T G G A G T G C T C T G G A G T T 8840 T C T G T C G G A A T T C T G T C G G A A T T C T G T C G G A A T T C T G T A T A A T 8890 A T G A C T A T A A T A A T G A C T A T A A T A T G A C T A T A A T	T A 2603_a12.seq A nem316_a12.seq C Majority 8850 C 2603_a12.seq C C nem316_a12.seq T T Majority 8900 T T 2603_a12.seq T T nem316_a12.seq
8617 8670 8667 8720	TGTTTCTCC TGTTTCTCCC GTCCGTTTG ATCCATTG GTCCGTTTG CTTTTTATA CTTTTTATA CTTTTTTATA	TACTTTACT TACTTTACT TACTTTACT BEIO TAGTTGATC TAGTTGATC TAGTTGATC TAGTTGATC ATCTCTTCA BEOO TATCTCTTCA	A A G A T A G T A C A A G A T A G T A C C C C A T T T A G C 8820 C C C C A T T T A G C C C C A T T T A G C G C A T T T A T T T G 8870 G C A T T A T T T G G C A T T A T T T G	T C C T T T T G T T T G C T T T T G T T 8830 T T T A G G A G C T T T A G G A G C T T T A A T T G T T T 8880 T T A A T T G T T T T A A T T G T T T	G C T C T G G A G T G C T C T G G A G T T S 8840 T C T G T C G G A A T C T G T C G G A A T C T G T C G G A A T C T G T A T A A T 8890 A T G A C T A T A A A T	T A 2603_a12.seq A nem316_a12.seq C Majority 8850 C 2603_a12.seq C C nem316_a12.seq T T Majority 8900 T T 2603_a12.seq T T nem316_a12.seq
8617 8670 8667 8720	TGTTTCTCC TGTTTCTCCC GTCCGTTTG ATCCATTG GTCCGTTTG CTTTTTATA CTCTGTCTG	TACTTTACT TACTTTACT TACTTTACT BEIO TAGTTGATC TAGTTGATC TAGTTGATC TAGTTGATC ATCTCTTCA BEOO TATCTCTTCA	A A G A T A G T A C A A G A T A G T A C C C C A T T T A G C 8820 C C C C A T T T A G C C C C A T T T A G C G C A T T T A T T T G 8870 G C A T T A T T T G G C A T T A T T T G	T C C T T T T G T T T G C T T T T G T T 8830 T T T A G G A G C T T T A G G A G C T T T A A T T G T T T 8880 T T A A T T G T T T T A A T T G T T T	G C T C T G G A G T G C T C T G G A G T B 840 T C T G T C G G A A T C T G T C G G A A T C T G T C G G A A T C T G T A G A A T G A C T A T A A A A T G A C T A T A A A A T G A C T A T A A A A T G A C T A T A A A A T T A A T C A T C T	T A 2603_a12.seq A nem316_a12.seq C Majority 8850 C 2603_a12.seq C C nem316_a12.seq T T Majority 8900 T T 2603_a12.seq T T nem316_a12.seq
8617 8670 8667 8720	TGTTTCTCC TGTTTCCCC GTCCGTTTG ATCCATTGC GTCCGTTTG CTTTTTATA CTCTGTCTG	TACTTTACT TACTTTACT TAGTTGATC 8810 TAGTTGATC TAGTTGATC ATCTCTTCA 8860 ATCTCTTCA ATCTCTTCA	A A G A T A G T A C A A G A T A G T A C C C C A T T T A G C 8820 C C C A T T T A G C C C C A T T T A G C G C A T T A T T T G G C A T T A T T T G C C C A T T A T T T G C T T A G T T T G A 8920	T C C T T T T G T T T G C T T T T G T T T G T T T G T T T G T T T G T T T G T T T G T T T G T T T T G T T T T T T T A A T T G T T T T	G C T C T G G A G T G C T C T G G A G T 8840 T C T G T C G G A A T C T G T C G G A A T T C A T C A T A A T A A T G A C T A T A A T A A T G A C T A T A A T A A T G A C T A T A A T A A T G A C T A T A A T A A T G A C T A T A A T A A T G A C T A T A A T A A T G A C T A T A A T A A T G A C T A T A A T A A T G A C T A T A A T A A T G A C T A T A A T A A T G A C T A T A A T A A T G A C T A T A A T A A T G A C T A T A A T A A T G A C T A T A A T	T A 2603_a12.seq A A nem316_a12.seq T C Majority 8850 T C 2603_a12.seq T C nem316_a12.seq T T Majority 8900 T T 2603_a12.seq T T nem316_a12.seq T T mem316_a12.seq T Majority
8617 8670 8667 8720	TGTTTCTCC TGTTTCCCC GTCCGTTTG ATCCATTGC GTCCGTTTG CTTTTTATA CTCTGTCTG	TACTTTACT CTACTTTACT CTACTTTACT 8810 CTAGTTGATC ATCTCTTCA 8860 ATCTCTTCA ATCTCTTCA ATCTCTTCA	A A G A T A G T A C A A G A T A G T A C C C C A T T T A G C 8820 C C C C A T T T A G C C C C A T T T A G C G C A T T A T T T G 8870 G C A T T A T T T G C C A T T A T T T G C T T A G T T T G A 8920 C T T A G T T T G A	T C C T T T T G T T T G C T T T T G T T T G T T T G T T T G T T T G T T T G T T T G G A G C T T G T A A T T G T T T T T A A T T G T T T T	G C T C T G G A G T G C T C T G G A G T T 8840 T C T G T C G G A A T T C T G T C G G A A T T C A T C A T C T 8890 A T G A C T A T A A T A A T A A T A A T A A T A T C A T C T 88940 A T T T A T C A T C T 8940 A T T T A T C A T C T A T A A T C A T C T T A T C A T C T C	T A 2603_a12.seq A nem316_a12.seq C Majority 8850 C 2603_a12.seq C C nem316_a12.seq C T Majority 8900 T T 2603_a12.seq C T nem316_a12.seq C T Majority 8950 C T Majority 8950 C T Z603_a12.seq C T Majority
8617 8670 8667 8720 8717	TGTTTCTCC TGTTTCCCC TGTTTCCCC GTCCGTTTG ATCCATTCG GTCCGTTTG CTTTTTATA CTTTTTATA CTCTGTCTG CTCTGTCTG CTCTGTCTG CTCTGTCTG	TACTTTACT TACTTTACT TAGTTGATC 8810 TAGTTGATC TAGTTGATC ATCTCTTCA 8860 ATCTCTTCA ATCTCTTCA AATTTGTGAA 8910 AATTGTGAA AATTGTGAA	A A G A T A G T A C A A G A T A G T A C C C C A T T T A G C 8820 C C C A T T T A G C C C C A T T T A G C G C A T T A T T T G 8870 G C A T T A T T T G G C A T T A T T T G C T T A G T T T G A 8920 C T T A G T T T G A	TT C T T T G T T T G C T T T T G T T T G C T T T T G T T 8330 TT T A G G A G C T T T A G G A G C T T T A A T T G T T T 8880 T T A A T T G T T T T A A T T G T T T T A A T T G T T T T A A T T G T T T A G G C C A T A A T 8930 A G G C C A T A A T A G G C C A T A A T	G C T C T G G A G T G C T C T G G A G T T T C T G G A A T T C A T C T A T A A T A T C A T C T A T A	T A 2603_a12.seq A nem316_a12.seq T C Majority 8850 T C 2603_a12.seq T C nem316_a12.seq T T Majority 8900 T T 2603_a12.seq T T nem316_a12.seq T T majority 8950 T T 2603_a12.seq T T majority
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		11710	11720	11730	•	•
11567	AGCTT	TTTAATCT			11740	11750
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	TTTTT	TECEATET	GAAATGTTCTT	TAATTCTTTT.	GCAATATTCT	G.T.T.G.T. Majority
		11760	-11770	11780	11790	11800
11617	TTTTT	TCCCATGT	GAAATGTTCTT	TAATTCTTT	1661171776	
11617	TTTTT	TCCCATGT	GAAATGTTCTT	TAATTCTTTT	A G C A A T A T T C T	GTTGT 2603_a12.seq GTTGT nem316_a12.se
	AGIII	CTCTCTTA	ATGCCTTATCT	TTTACTAATA	ATCAAGAGAT	TCATG Majority
		11810	11820	11830	11840	11850
11667	AGTTT	CTCTCTTA	ATGCCTTATCT	TTTACTAATA	1 4 7 0 1 1 0 1 0 1	
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	O K O I U		LITICITECAT	GATGATTCCT	ACTCAGGGCT	ATCAA Majority
		11860	11870	11880	11890	11900
11717	GAGTG	ACTGAGTA	TTTTCTTCCAT	GATGATTCCT	ACTCAGGGCT	ATCAA 2603_ai2.seq
11/1/	GAGTG	ACTGAGTA	TTTTCTTCCAT	GATGATTCCT	ACTCAGGGCT	ATCAA 2603_ai2.seq ATCAA nem316_ai2.seq
				CTGTTGCAATA	ATAGCACTTG	A A G T Majority
	•	11910	11920	11930	11940	. 11950
11767	TAACT	TCAACTGT	TCCACCGCGAT	CTGTTGCAATA	ATAGCACTTG	A A A G T 2603_a12.seq
111,01	TAKCI	ICAACTGT:	TCCACCGCGAT	CTGTTGCAATA	ATAGCACTTG	AAAGT 2603_ai2.seq AAAGT nem316_ai2.seq
				GGTAATCCCTC		
		11960			•	G A A G G Majority
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11817	AGACC	A G C T T C T A .	AAATAGÁGGTT	GGTAATCCCCTC	TGGATACATT	G A A G G 2603_a12.seq
	, a G a C C Z	. O.C.I.C.I.K.	AAAIAGAGGTT	GGTAATCCCTC	TGGATACATT	GAAGG 2603_ai2.seq GAAGG nen316_ai2.seq
	GTAAAC	CAAAGATAT	CAGTCTGTGC	CATTAAAGACA	TAGTCTCTTC	A A A C T Wolontes
		12010	12020	12030	•	• •
11867	GT A A A.C	CANAGATAS			12040	12050
11867	GTAAA	AAAGATAT	CAGTCTGTGC	CATTAAAGACA CATTAAAGACA	TAGTCTGTTC	A A A G T 2603_a12.seq A A A G T nem316_a12.seq
	TTAATI	TCCCCAAA	AAGTTAATCT	G T T T G G A C T C A	TATTTCTCTT	
		COOOKA		O I I O O N O I O N	ARILLOLU I	I C A A A Majority
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11911	TTAATI	12060	12070	12080 CTTTCCACTCA	12090	12100
11917	TTAATI	12060	12070	12080 CTTTCCACTCA	12090	12100
11917	T T A A T 1	TCCCCAAA	12070 AAGTTAATCT AAGTTAATCT	12080 G T T T G G A C T G A G T T T G G A C T G A	12090 TATTTCTCTTT	12100 T C A A A 2603_a12.seq T C A A A nem316_a12.seq
11917	T T A A T 1	12060 TTCCCCAAA TTCCCCAAA	12070 AAGTTAATCT AAGTTAATCT	12080 CTTTCCACTCA	12090 TATTTCTCTTT	12100 T C A A A 2603_a12.seq T C A A A nem316_a12.seq
	TTAATI TTAATI	12060 TTCCCCAAA TTCCCCAAA AATTCAGG	12070 A A G T T A A T C T A A G T T A A T C T C T C C G T C T C C T 12120	12080 G T T T G G A C T G A G T T T G G A C T G A G T T T G G A C T G A A T C T G T A A 12130	12090 TATTTCTCTTT TATTTCTCTTT ATAAACATTT	12100 T C A A A 2603_a12.seq T C A A A nem316_a12.seq F C A G A Majority 12150
11967	TTAATT TTAATT TGTGCT	12060 TTCCCCAAA TTCCCCAAA AATTCAGG 12110	12070 A A G T T A A T C T A A G T T A A T C T C C G T C T C C T 12120	12080 G T T T G G A C T G A G T T T G G A C T G A G C A A T C T G T A A 12130	12090 TATTTCTCTT TATTTCTCTT ATAAACATTT	12100 T C A A A 2603_a12.seq T C A A A nem316_a12.seq F C A G A Majority 12150
11967	TTAATT TTAATT TGTGCT	12060 TTCCCCAAA TTCCCCAAA AATTCAGG 12110	12070 A A G T T A A T C T A A G T T A A T C T C C G T C T C C T 12120	12080 G T T T G G A C T G A G T T T G G A C T G A G C A A T C T G T A A 12130	12090 TATTTCTCTT TATTTCTCTT ATAAACATTT	12100 T C A A A 2603_a12.seq T C A A A nem316_a12.seq F C A G A Majority 12150
11967	TTAATTTTAATTTTAATTTTAATTTTTAATTTTTTTTT	12060 TTCCCCAAA TTCCCCAAA AATTCAGG 12110 TAATTCAGG	12070 A A G T T A A T C T A A G T T A A T C T B T C C G T C T C C T 12120 B T C C G T C T C C T C T C C G T C T C C T	12080 G T T T G G A C T G A G T T T G G A C T G A G C A A T C T G T A A 12130 G C A A T C T G T A A G C A A T C T G T A A	12090 TATTTCTCTTT TATTTCTCTTT ATAAACATTT 12140 ATAAACATTT ATAAACATTT	12100 T C A A A 2603_a12.seq T C A A A nem316_a12.seq T C A G A Majority 12150 T C A G A 2603_a12.seq T C A G A nem316_a12.seq
11967	TTAATTTTAATTTTAATTTTAATTTTTAATTTTTTTTT	12060 TTCCCCAAA TTCCCCAAA AATTCAGG 12110 TAATTCAGG AATTCAGG TGACATCG	12070 A A G T T A A T C T A A G T T A A T C T ET C C G T C T C C T E2120 ET C C G T C T C C T ET C C G T C T C C T	12080 G T T T G G A C T G A G T T T G G A C T G A G C A A T C T G T A A 12130	12090 TATTTCTCTTT TATTTCTCTTT ATAAACATTT 12140 ATAAACATTT ATAAACATTT	12100 T C A A A 2603_a12.seq T C A A A nem316_a12.seq T C A G A Majority 12150 T C A G A 2603_a12.seq T C A G A nem316_a12.seq
11967 11967	TTAATTTTAATTTTAATTTTAATTTTTAATTTTTTTTT	12060 T C C C C A A A T C C C C A A A A A T T C A G G 12110 T A A T T C A G G A A T T C A G G T G A C A T C G	12070 A A G T T A A T C T A A G T T A A T C T T C C G T C T C C T 12120 T C C G T C T C C T T C C G T C T C C T A A A A T G C T T C 12170	12080 G T T T G G A C T G A G T T T G G A C T G A G C A A T C T G T A A 12130 G C A A T C T G T A A G C A A T C T G T A A T A A G A G C A A T T 12180	12090 TATTTCTCTTT TATTTCTCTTT ATAAACATTT 12140 ATAAACATTT ATAAACATTT CAATCCTTTT	12100 T C A A A 2603_a12.seq T C A A A nem316_a12.seq T C A G A Majority
11967 11967	TTAATT TTAATT TGTGCT TGTGCT GTACTG	12060 T C C C C A A A T C C C C A A A A A T T C A G G 12110 T A A T T C A G G A A T T C A G G T G A C A T C G 12160 T G A C A T C G	12070 A A G T T A A T C T A A G T T A A T C T 12120 T C C G T C T C C T T C C G T C T C C T A A A A T G C T T C L2170	12080 G T T T G G A C T G A G T T T G G A C T G A G C A A T C T G T A A 12130 G C A A T C T G T A A G C A A T C T G T A A T A A G A G C A A T T 12180	12090 TATTTCTCTT TATTTCTCTT ATAAACATTT 12140 ATAAACATTT ATAAACATTT CAATGCCTTT 12190	12100 T C A A A 2603_a12.seq T C A A A nem316_a12.seq T C A G A Majority
11967 11967	TTAATT TTAATT TGTGCT TGTGCT GTACTG	12060 TTCCCCAAA TTCCCCAAA AATTCAGG 12110 TAATTCAGG TGACATCG 12160 TGACATCG	12070 A A G T T A A T C T A A G T T A A T C T 12120 T C C G T C T C C T T C C G T C T C C T A A A A T G C T T C L2170	12080 G T T T G G A C T G A G T T T G G A C T G A G C A A T C T G T A A 12130 G C A A T C T G T A A G C A A T C T G T A A T A A G A G C A A T T 12180	12090 TATTTCTCTT TATTTCTCTT ATAAACATTT 12140 ATAAACATTT ATAAACATTT CAATGCCTTT 12190	12100 T C A A A 2603_a12.seq T C A A A nem316_a12.seq T C A G A Majority 12150 T C A G A 2603_a12.seq T C A G A nem316_a12.seq T C A G A Majority
11967 11967	TTAATTTTAATTTTAATTTTAATTTTTAATTTTTTTTT	12060 TTCCCCAAA TTCCCCAAA AATTCAGG 12110 AATTCAGG AATTCAGG TGACATCG TGACATCG TGACATCG	12070 A A G T T A A T C T A A G T T A A T C T 12120 T C C G T C T C C T T C C G T C T C C T T C C G T C T C C T A A A A T G C T T C A A A A T G C T T C A A A A T G C T T C	12080 G T T T G G A C T G A G T T T G G A C T G A 12130 G C A A T C T G T A A 12130 G C A A T C T G T A A G C A A T C T G T A A 12180 T A A G A G C A A T T T A A G A G C A A T T	12090 TATTTCTCTTT TATTTCTCTTT ATAAACATTT 12140 ATAAACATTT ATAAACATTT CAATGCCTTTT 12190 CAATGCCTTTT CAATGCCTTTT	12100 T C A A A 2603_a12.seq T C A A A nem316_a12.seq T C A G A Majority 12150 T C A G A 2603_a12.seq T C A G A nem316_a12.seq T C T T Majority 12200 T T C T T 2603_a12.seq T T C T T nem316_a12.seq
11967 11967	TTAATTTTAATTTTAATTTTAATTTTTAATTTTTTTTT	12060 T C C C C A A A T C C C C A A A A A T T C A G G 12110 A A T T C A G G A A T T C A G G T G A C A T C G T G A C A T C G T G A C A T C G	12070 A A G T T A A T C T A A G T T A A T C T 12120 T C C G T C T C C T T C C G T C T C C T A A A A T G C T T C A A A A T G C T T C A A A A T G C T T C A A A A T G C T T C A A A A T G C T T C A A A A T G C T T C A A A A T G C T T C A A A A T G C T T C A A A A T G C T T C	12080 G T T T G G A C T G A G T T T G G A C T G A G C A A T C T G T A A 12130 G C A A T C T G T A A C C A A T C T G T A A I A A G A G C A A T T I A A G A G C A A T T I A A G A G C A A T T I A A G A G C A A T T	12090 TATTTCTCTTT TATTTCTCTTT ATAAACATTT 12140 ATAAACATTT ATAAACATTT ATAAACATTT CAATCCTTT 12190 CAATCCTTTT CAATCCTTTT CAATCCTTTT CAATCCTTTT	12100 T C A A A 2603_a12.seq T C A A A nem316_a12.seq T C A G A Majority 12150 T C A G A 2603_a12.seq T C A G A nem316_a12.seq T C T T Majority 12200 T T C T T 2603_a12.seq T T C T T nem316_a12.seq
11967 11967 12017 12017	TTAATT TTAATT TGTGCT TGTGCT GTACTG GTACTG	12060 T C C C C A A A T C C C C A A A A A T T C A G G 12110 A A T T C A G G A A T T C A G G T G A C A T C G T G A C A T C G T G A C A T C G T G A C A T C G	12070 A A G T T A A T C T A A G T T A A T C T 12120 T C C G T C T C C T T C C G T C T C C T T C C G T C T C C T A A A A T G C T T C A A A A T G C T T C G C A T A A G T G A T 12220	12080 G T T T G G A C T G A G T T T G G A C T G A 12130 G C A A T C T G T A A 12130 G C A A T C T G T A A G C A A T C T G T A A T A A G A G C A A T T T A A G A G C A A T T T A A G A G C A A T T T A A G A G C A A T T T A A G A G C A A T T T A A G A G C A A T T	12090 TATTTCTCTTT TATTTCTCTTT ATAAACATTT 12140 ATAAACATTT ATAAACATTT CAATCCTTT 12190 CAATCCCTTT CAATCCCTTT TCAGCAGATTT 12240	12100 T C A A A 2603_a12.seq T C A A A nem316_a12.seq T C A G A Majority 12150 T C A G A 2603_a12.seq T C A G A nem316_a12.seq T T C T T Majority 12200 T T C T T 2603_a12.seq T T C T T nem316_a12.seq T T C T A Majority 12250
11967 11967 12017 12017	TTAATT TTAATT TGTGCT TGTGCT GTACTG GTACTG TAATAA	12060 TTCCCCAAA AATTCAGG 12110 AATTCAGG AATTCAGG 12160 TGACATCG TGACATCG TTCTACCA 12210 TTCTACCA	12070 A A G T T A A T C T A A G T T A A T C T 12120 T C C G T C T C C T T C C G T C T C C T T C C G T C T C C T A A A A T G C T T C A A A A T G C T T C G C A T A A G T G A 12220. G C A T A A G T G A	12080 G T T T G G A C T G A G T T T G G A C T G A 12130 G C A A T C T G T A A 12180 T A A G A G C A A T T T A A G A G C A A T T T A A G A G C A A T T T A A G A G C A A T T T A A G A G C A A T T T C A A A A T A T C A	12090 TATTTCTCTTT TATTTCTCTTT ATAAACATTT 12140 ATAAACATTT ATAAACATTT ATAAACATTT CAATGCCTTTT 12190 CAATGCCTTTT CAATGCCTTTT CAATGCCTTTT TCAGCAGATTT	12100 T C A A A 2603_a12.seq T C A A A nem316_a12.seq T C A G A Majority 12150 T C A G A 2603_a12.seq T C A G A nem316_a12.seq T C T T Majority 12200 T T C T T 2603_a12.seq T T C T T nem316_a12.seq T T C T T nem316_a12.seq T T C T A Majority
11967 11967 12017 12017	TTAATT TTAATT TGTGCT TGTGCT GTACTG GTACTG TAATAA	12060 TTCCCCAAA AATTCAGG 12110 AATTCAGG AATTCAGG 12160 TGACATCG TGACATCG TTCTACCA 12210 TTCTACCA	12070 A A G T T A A T C T A A G T T A A T C T 12120 T C C G T C T C C T T C C G T C T C C T T C C G T C T C C T A A A A T G C T T C A A A A T G C T T C G C A T A A G T G A 12220. G C A T A A G T G A	12080 G T T T G G A C T G A G T T T G G A C T G A 12130 G C A A T C T G T A A 12180 T A A G A G C A A T T T A A G A G C A A T T T A A G A G C A A T T T A A G A G C A A T T T A A G A G C A A T T T C A A A A T A T C A	12090 TATTTCTCTTT TATTTCTCTTT ATAAACATTT 12140 ATAAACATTT ATAAACATTT ATAAACATTT CAATGCCTTTT 12190 CAATGCCTTTT CAATGCCTTTT CAATGCCTTTT TCAGCAGATTT	12100 T C A A A 2603_a12.seq T C A A A nem316_a12.seq T C A G A Majority
11967 11967 12017 12017 12017	TTAATT TTAATT TGTGCT TGTGCT GTACTG GTACTG TAATAA TAATAA	12060 T C C C C A A A T C C C C A A A T C C C C A A A A T T C A G G 12110 A A T T C A G G A A T T C A G G T G A C A T C G T G A C A T C G T G A C A T C G T G A C A T C G T G A C A T C G T T C T A C C A T T C T A C C A	12070 A A G T T A A T C T A A G T T A A T C T 12120 T C C G T C T C C T T C C G T C T C C T A A A A T G C T T C A A A A T G C T T C A A A A T G C T T C G C A T A A G T G A T G C A T A A G T G A T G C A T A A G T G A T	12080 G T T T G G A C T G A G T T T G G A C T G A G C A A T C T G T A A 12130 G C A A T C T G T A A G C A A T C T G T A A I A A G A G C A A T T I A A G A G C A A T T I A A G A G C A A T T I A A G A G C A A T T I A A G A G C A A T T I A A G A G C A A T T I C A A A A T A T C A I C G A A A A T A T C A	12090 TATTTCTCTTT TATTTCTCTTT ATAAACATTT 12140 ATAAACATTT ATAAACATTT ATAAACATTT CAATCCTTT 12190 CAATCCCTTT CAATCCTTT CAATCCTTT TCAGCAGATTT 12240 TCAGCAGATTT TCAGCAGATTT	12100 T C A A A 2603_a12.seq T C A A A nem316_a12.seq T C A G A Majority
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TTCTCTTAGGATAGGCGGT Majority 12360 12370 12380 12390 12400 12217 TTCTCTTGGATACCGCATAAAATCTGGACGATAATGCTTAACACGCGCT 2603_at2.seq 12217 TTCTCTTGGATACCGCATAAAATCTGGACGATAATGCTTAACACGCGCT nem316_a12.seq GTGAGAAGATGTTCATAGATAGCTCCAAAGAAATCTAAAAAACGATTATT Majority 12410 12420 12430 12440 12450 12267 GTGAGAAGATGTTCATAGATAGCTCCAAAGAAATCTAAAAAACGATTATT 2603_a12.seq
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	TTTT	ATA	A.T.A.T.A	GATEG	C A. ToT, G	CGTAT	CATGTA	ATATT	TTCGAAA	TGGTG Majority
	+	p 4	13010		13020		13030		13040	13050
12867	'	ATA	ATATA	GATCG	CATTG	CGTAT	CATGTA	ATATI	TTCGAAA	T G G T G 2603_a12.seq
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	AATG	ATT	CAATA	CATGA	AAAAC	ATGGC	CAAATT	TTTTA	ACTCGTG	A A G A G Majority
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12917	' AATG. ' AATG	ATT	CAATA	CATGA.	A A A A C	ATGGC	CAAATT	TTTTA	ACTCGTG	GAAGAG 2603_a12.seq GAAGAG nem316_a12.seq
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	TGTC	CAA		TGTAA	CAGAC	CAATA	ATTA	ACCTG	ATAAGTC	TTATA Majority
			13110		13120 -		13130		13140	13150
12967	TGTC		TTTCG TTTCG	TGTAAC		CAATA.	AAATTA	ACCTG	ATAAGTO	CTTATA 2603_a12.seq CTTATA nem316_a12.seq
	TCCC	A T C		CAGACO		TTCAT	T.T C A G A	G T C A A	CAAAATC	AATAA Majority
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13017	TCCC	ATC'	T C T G A		G A T A A G A T A A	TTCAT	TTCAGA	GTCAA	CAAAATC	AATAA 2603_a12.seq AATAA nem316_a12.seq
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	ACAIC	. <u>1 U</u>		CAAAG		TGTTT	•	A A A C·G	CTCGTTT	TCATT Majority
. 12007	ACATO	C T C .	13210		13220		13230		13240	13250
13067	ACAT	CTC.	TTCTG	C A A A G (CAGA	TGTTT	CTT'CGA CTTCGA	A A A C G A A A C G	CTCGTTT	TCATT 2603_a12.seq TCATT nem316_a12.seq
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13117	A A.A G C	CAG		GTAATA		CTTCL	13280	T T 4 T 4	13290	13300 TCTTG 2603_a12.seq
13117	AAAG	AG	CCGAA	GTAAT	CACT	CTTCA	TTTCT	 	GTCAAAT	TCTTG 2603_a12.seq TCTTG nem316_a12.seq
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•		·. ·.	13310		13320		13330		13340	13350
13167	CATCA	C.T	AATT	TTCACO	GTTC	ATATCT	FFGATA	CAAAC	AACATAA	C A T A C 2002 -12
13167	CATCA	CT	TTAK	TTCAC.	GTTC	A'T·ATC7	TGATA	CAAAC	AAGATAA	CATAC nem316_a12.seq
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			13360	•	13370	•	13380		13390	13400
13217	CGACC	TT	GGTA	AATGAA	GGTA	ATTTT	ATAAT	FATCT	ATCAAAT	C A C C T 2603_a12.seq
13217				•						CACCT nem316_ai2.seq
	AGGAC	AAC	CGAAT	CTTGA	T.CTA	AAGTCA	AGAACO	CAATC	AAATTCT	TGTGC Majority
			13410		13420		13430	·	13440	. 13450
13267 13267	AGGAC		C G A A 1 C G A A 1	T C T T G A T C T T G A	ТСТА.	A A G T C A	AGAAC	CAATC	AAATTCT	TGTGC 2603_ai2.seq TGTGC nem316_ai2.seq
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10015			13460		13470	<u>:</u>	13480		13490	13500
13317	TACTG	CAA	ATTG	A C C G A T A C C G A T	ACAG	TTCAAA TTCAAA	GCATAT		TCCCTTT	ATTTT 2603 a12 seq ATTTT nem316 a12 seq
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	<u>CIG:14</u>	A A A	13510	XACAG		TCCCC		•	TAATCGG	CTACT Vajority
13367	CTCTT	A A A		1'4 C'4 C	13520	20000	13530		13540	13550
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13417	AATTG	AGA	<u> </u>	CTTCC	1	· • T T T C C	•		13590	13600 TAGAT 2603_a12.seq
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			13610		13620	<u> </u>	13630		13640	13650
13467	GTGGC	TTA	'1	GGATA		CTCGA				T T C A A 2603_ai2.seq
13467	GTGGC	TTA	CTTGA	GGATA	AATT	CTCGA	ATCTTC	TGAT	CTAAGCG	TTC

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- Thurs	oay, July 29, 230, 8,55					1 0 17 0 5 2 0
	TCACG,A,A,T	AGGAGCTT	GG XIG E ALA CIT	TAGCATCCCC	CTGAACCAGAAAC	Majority
•	Han Hanta	660 July 1001, 1001, 1001	670	680		
651	TCACCAAT	ACCACCTTO				
-651	TCACGAAT	AGGAGGTTCT	I G G A G C A A C T	ATAGCATCCCC	CTGAACCAGAAAC	cohl_a12.seq
			IGGAGCAACI	AIAGCATCCCC	CTGAACCAGAAAC	a909_a12.seq
	TGTGCAAA	AAGTGCACCC	TCCTCTAGC.	AACTGTTCCAT	CTCTGTTAGGAC	Wa. 1 15
		710				Majority
			720 .	730	740 75	
701 701	TGTGCAAA	AAGTGCACC	CTCCTCTAGC	AACTGTTCCAT	CTCTGTTAGGAC	cohi_ai2.seq
701	IGIGCAAA	AAGTGCACC	CTCCTCTAGC.	AACTGTTCCAT	CTCTGTTAGGAC	a909_a12.seq
	AGTCAAAA	CCAGCATCTA	. T. A. C. C. T. A. T. T.	T		-
				LAAALAITTI	TCTCCAAAGAGT	Majority
٠.		760	770	780	790 80	0
751	AGTCAAAA	CCAGCATCTA	TAGGTAATT	TAAATATTTT	TTCTCCAAAGAGT	cohi al2 seg
751	AGTEAAAA	CCAGCATCTA	TAGGTAATT	ΤΑΑΑΤΑΤΤΤΊ	TTCTCCAAAGAGT	a909 a12 seq
•	•					
	1 C I C G K I K	AIAAICAIIA	AICGCACGA	<u> </u>	CATAGGATAATT	Majority
	·.	. 810	820	830	840. 856))
801	TCTCGATA	ATAATCATTA	ATCGCACGA	TAACGTTTTT	CATAGGATAATT	
801	TCTCGATA	ATAATCATTA	ATCGCACGA	TAACGTTTTT	CATAGGATAATI	2909 a12 seq
	GTATCACA	ATTTTAACTA	AAATAACCTO	CACTACTACAA	TAAAACTAAAAA	Majority
		860 -	870	880	890 900	
851	GTATCACA	ATTTTAACTA	AAATAACCTA	CACTACTACA	TAAAACTAAAAA	
851	GTATCACA	ATTTTAACTA	AAATAACCI	CACTACTACAA	A A A A A T A A A A A A A A A A A A A A	cohi_ai2.seq
	AGATTGGA	ACGTCAGTTA	GTTCCAATCT	TTTATTACT	TCACTTTCTTTA	Valority
٠.		910	920	930	•	=
901	ACATTCCA	FCCTCLCTT				
901	AGATTGGA	ACCTCACTTA	CTTCCAATCT	TTTATTACT TTTTATTACT	TCACTTTCTTTA	cohl_a12.seq
•	_		•			a909_a12.seq
	ACCAATCC	TTGGCTAAAA	AGATATACGO	CAGTTAGATTC	AAAATACCATAA	Majority
	•	960	970	980	•	
951	ACCAATCC	1.				
951	ACCAATCC	TTCCCTAAAA	AGATATACGC		A A A A T A C C A T A A A A A A T A C C A T A A	cohl_a12.seq
		IIGUUIAAA	A GAIA.IACGC	AGIIAGATTO	AAAATACCATAA	a909_ai2.seq
	GCAAGTAT	AAAACCAGCT	AAAACATCTG	TCGGAAAATG	AACCCCTAGGTA	Valority
		1010	1020	•		=
1001				1030	1040 1050	
1001	GCAAGTAT.	AAAACCAGCT	AAAACATCTG	TCGGAAAATG	AACCCCTAGGTA	coh1_ai2.seq
1001	CCARGIAI	A A A A C C A G C 1	AAACATCTG	TCGGAAAATG	AACCCCTAGGTA	a909_a12.seq
	AATACGAGA	ATAACCCAAT	TAAAAAAATG	AGCAAACCCA	ATGTA:CCTTGGC	W-1
		1060			•	
***	·	<u> </u>	1070	1080	1090 1100	
1051	AATACGAGA	ATAACCCAAT	TAAAAAAATG	AGCAAACCCA	ATGTACCTTGGC	coh1_ai2.seq
1051	AAIACGAGA	ATAAUUUAAT	TAAAAAAATG	A G C A A A C C C A	AATACCTTGGC	a909_a12.seq
	ACAACAGTT	TTCCATATAC	T C T T A C C C A T	AT'ACTACTCC	AATAAAATAATA	
				-	AAIAAAIAATA	Majority
. •		1110	1120	1130	1140 1150	
1101	ACAACAGTT	TTCCATATAC	TCTTAGGCAT	ATAGTACTGC	AATAAAATAA	cohl ai2.sea
1101	ACAACAGT	TTCCATATAC	TCTTAGGCAT	ATAGTACTCC	AATAAAATAATA	a909_a12.seq
•				_		
	CIACICCEA	AAAAALCATA	AATGTTCECA	TCGACTCCCC	A C T G G G A A A C G A	Najor i ty
. •		4160	1170	1180	1190 1200	,
1151	CTACTCCC	AAATATCATA	AATGTTCCCA	TCGAGTCCCC	ACTGGGAAACGA	
1151	ATACT CCC/	AAATATCATA	AATGTTCCCA	TEGAGTGCCC	A-C T G G G A A A C G A	coni_aiz.seq
		•		•	•	
	ATAGCCACC	CTGCAAATAC	TAAATGGGTT	AAAGTTGGTC	TCACTCTTTGAA	Majority
,		1210	1220	1230		·
1201			•			
1201	ATAGCCACC	O L U U A A A A A A A A A A A A A A A A A	1 A A A T C C C T T	AAAGTTGGTC	TCACTCTTTGAA	cohl_ai2.seq
	" i vac o vac	O A U C A A A A A C.	IAAAIGGGTT	AAAGTTGGTC	TCACTCTTTGAA	a909_a12.seq
	AAATAAGTT	TTAAAGAAA	G T A T A C A T A T	ACCARAGATA	ATAGCATTTACT	Valorit
				-		
	·	•	1270	1280	1290 1300	
125'I 125'I	AAATAAGTT	TTAAAGAAA	GTATACATAT	ACCAGAGATA	A T A G C A T T T A C T A T A G C A T T T A C T	cohl_ai2.seg

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Aligna	nent Report of WO 200 day, July 29, 2004 0:49 Fi	06/078318 in meth	og with Weighted residue			PCT/US20
			A G-G-A-T-A C-C-A-C	TTCTTAAGGT	AACAGAAAGTGA	C Majority
		1310	1320	1330	•	1350
1301 1301	G C G A T A A A T G C G A T A A A T	CTAGCTTG CTAGCTTG	A G G A T A C C A C A G G A T A C C A C	T T C T T A A G G T T T C T T A A G G T	A A C A G A A A G T G A A A C A G A A A G T G A	. C cohi_ai2.seq
•					CCAACCACAGTG	-
]	1360	1370	1380		1400
1351 1351	G C T C A T A A T G C T C A T A A T		C T A T C T G G C T C T A T C T G G C T	TACAGTATTA TACAGTATTA	C C A A C C A C A G.T G C C A A C C A C A G T G	A cohl_ai2.sèq A a909_ai2.seq
	TTAACTTGA				TCCTCTAACACT	
. :		410	1420	1430	1440	1450
1401 .1401	TTAACTTAA	A A A A T C T T	G T A G A A A G A T G T A G A A A G A T	TTGGCAACTG TTGGCAACTG	T C C T C T A A C A C T T C C T C T A A C A C T	T cohl_ai2.seq
	TCTTGAATA		•		GCCAATATTTGA	•
		460	1470	1480	1490	1500
1451 1451	T C T T G A A T A	GTTTGGTC	A A A T G C G A T T	A C A G T G T C G G	G C C A A T A T T T G A G C C A A T A T T T G A	T cohi_ai2.seq
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:	•	510	1520	1530	AATGETTGAATA 1540	A Majority (550
1501	GACCAATCC	TAAACTGA	AAAATAAGAT	AATAGCAATA	AATGCTTGAATA	A cobt at2 con
1501					AATGCTTGAATA	-
•		TTTGACGAC	· •		ATCTTTCTAATA	
.1551		<u> </u>	ISTO	1580 GTCTTTTAT.		1600
1551	GTTTACTAT	TTTGACGA	GATAACATTA	GTCTTTTTAT	A T C T T T C T A A T A	T cohl_ai2.seq T a909_ai2.seq
	TGGCAAACA	AGCCACGTA	AGTTAGATA	GAAACAATC	G A.A A T T A A A A T T.	C Kajority
1601		610	1620	1630		650
,1601	TGGCAAACA	AGCCACGTA	A A G T T A G A T A C	G A A A A C A A T C (G A A A A C A A T C (G A A A T T A A A A T T G A A A T T A A A A T T	C cohl_ai2.seq C a909_ai2.seq
				•	G T A A T T G C C T A C.	_
•	10	660	1670	1680	1690 1	700
1651 1651		T A T T A A A T (G A A T A A C C A T	T T G T T A A A A G (T T G T T A A A A G (G T A A T T G C C T A C G T A A T T G C C T A C	A cohi_ai2.seq A a909_ai2.seq
			,		CATACAAAGGAA	_
	1:	710	1720	. 1730	1740. 1	750
1701 1701		GTTCTGATA GTTCTGATA	A T C A A A G T T A C	G C A A A T A T A G (G C A A A T A T A G (C A T A C A A A G G A A C A T A C A A A G G A A	T cohl_ai2.seq T a909_ai2.seq
					AAGCTAACTGTA	
		760	1770	1780	1790 1	800 .
1751 1751	CGCAAAGAC	ATAGTTGAG ATAGTTGAG	AGCTACCAT	GATACAGTCA	A A G C T A A C T G T A A A G C T A A C T G T A	C cohl_ai2.seq
T 17 3 4 4					CCTATTTTTCCA	
··	•	310	1820	1830		<u>G</u> Kajority . 850
1801	CAAATAAAC	TAGCTTTAA	TAAAATCTT	TTGCACTCTCT	CCTATTTTCCA	C cohi at2 com
1801					CTATTTTCCA	•
<i>:</i> .	•			•	CATATTCATCG	4."
1851	*	AAACTTGCT	1870	1880 .	1890 - 19 CCATATTCATCG	900
1851	AAAATAGCG	AAACTTGCT	AAAAATAGAG	CTAGAGCAAC	CCATATTCATCG	G a909_a12.seq
	TAAACCGATA	AAGGTTTC	TGGACCACGA	TTAGCAAGTA	LTAACTTTTAAA.	A Majority
anc's		10	1920	1930	1940 19	950
1901 1901	TAAACCGAT	A	T G G A C C A C G A T G G A C C A C G A	TTAGCAAGTA TTAGCAAGTA	T A A C T T T T A A A A C T T T T A A A	A cohl_ai2.seq
	_	. •				

Thurs	day, July 29, 2W U				g					PC1/US20
-	GTGAT,CT	TAATA	A G.A GT	A C.A.C.C	A THA ANG	TTGATT	TCAAA	TCAAAT	AAAATA	Majority
	ll Har	1960	and death death sea	1970	,p' there end!	1980		1990 .	2000	•
1951	GTGATCT	TAATA	AGAGT	ACACO	ATAAC		FECAAA			
1951	GTGATCT	TAAT	AGAGT	ACAC	CATAAC	TTGAT	T C A A-A	TCAAAT		coni_ai2.seq
										=
	AAAGCAA	CTAAC	ATCGG	AAGGA	TTGAA	AAATCA	ACCTT	TAAAAA	TTCTGC	Majority
		2010	•	2020		2030	• •	2040	2050	o
2001	AAAGCAA	CTAAC	ATCGG	AAGGA	TTGAA	AAATCA	ACCTT	TAAAAA	TTCTCC	cobl. al2 coa
2001	AAAGCAA	CTAAC	ATCGG	AAGGA	TTGAA	AAATCA	ACCTT	TAAAAA	TTCTGC	a909_ai2.seq
_										
:	TCCTGGT		TO O X X		RCCAI	•	IACAA	•	AGGCAG	Majority
		2060		2070		2080		2090	2100	
2051 2051	TCCTGGT	A T T A A	TGGAA	ATGAA	ACCAT	CATCAA	TACAA	A A.G A T A	AGGCAG	cohi_at2.seq
.2031	TCCTGGT.	KIIAA	. I G G A A	AIGAA	ACCAT	CATCAA	TACAA	AAGATA	AGGCAG	a909_a12.seq
	AAAGAAT	GGCGA	TTGTC	A'C C A T	TTTAC	GTGTAT	TTGTC	A T A A A A	AAATTC	Majority .
•		2110	-	2120		2130	•	2140		
2101	AAAGAAT	G C C A	TTCTC		T T T A O				2150	
2101	AAAGAAT	G.G C G A	TTGTC	A C.C A T	TTTAC	G T G T A T	TTGTC	ATAAAA	AAATTC	cohl_ai2.seq
						•	•			
	CTCCAATI	<u> </u>	TAAAT	TGAAA	GAAGC	TCCAAA	GGTAA	GCGTAG	GTACGC	Majority
·	. • •	2160		2170		2180		2190	2200)
2151	CTCCAAT	TAAA	T.A.A.A.T	TGAAA	GAAGC	TCCAAA	GGTAA	GCGTAG	GTACEC	cohi at2 can
2151	CTCCAAT	ГТААА	TAAAT	TGAAA	GAAGC	TCCAAA	GGTAA	GCGTAG	GTACGC	a909_ai2.seq
					-				-	
	GAAAAAA		16161	•••	CAICC		TACTG	TCGGTT	GTGGAA	Majority
:		2210	·	2220		2230		2240	2250	
2201	GAAAAAA	CCTT	TGTCT	TCTCC	CATCC	A G A C T.T	TACTG	TCGGTŤ	GTGGAA	coh1_ai2.seq
2201	GAAAAAA	. CCII	IGTOT	T C T C C	CATCC	AGACTT	TACTG	TEGETT	GTGGAA	a909_a12.seq
	TCTCACCA	CATC	AGCTT	T C G C T	CGCGG	ACTGAT	GCTTC	ACAACT	GAC.AAA	Valority .
•		2260		2270		2280		2290		
2251	TCTCACCI		ACCTT		0.000			• .	2300	
2251	TCTCACC	CATC	AGCTT	T C G C T	00000	A C T G A T	GCTTC	A C A A C T	GACAAA	cohl_al2.seq
		•	-		-				•	•
	TAAGTTGG	AAGE	GATTAC	<u>c c ç c c</u>	GGTCG	C C A A T T	ACACC	CTGCCC	TGAAGA	Kajority '
		2310		2320	-	2330		2340	2350	
2301	TAAGTTGG	AAGC	GATTA	CCGCC	GGTCG	GGAATT	ACACC	CTGCCC	T G A· A G· A	cohl al2 sen
2301	TAAGTTGG	AAGC	GATTA	CCGCC	GGTCG	GGAATT	AGACC	CTGCCC	TGAAGA:	a909_a12.seq
	CACCTATA	GCAT	AACAA		ACTTG		C A A C T	TTTTT 1		er. e
		2360		•	X O I I G	• •	CAAGI			
2251	0.4.0.0.0.0.0.0.0			2370		2380	<u> </u>	2390	2400	
2351 2351	CACCTÁTA	GCAT	AACAA		ACTTG	CAATTG	CAAGE	TTTTTA	ATCACT	cohl_a12.seq
	CACCTATA	GUAL	A A C A A A		ACTIG	CAAIIG	CAAGT	TITTTA	ATCACT	å909_a12.seq
	<u>ÁATTAGTA</u>	GTAG	ATTGTA	TAAT	ATTAA	A'TTTT	ACATC	AATTAA	TTGACA !	Majority
		2410		2420		2430		2440	2450	, , , ,
2401	AATTAGTA	GTAG	ATTGT	TAAT	ATTAA		A C A T C			-264 -10 -2
2401	· A A T T A G T A	G T A G	ATTGT	TAAT	ATTAA	TTTTTA	ACATO		TTGACA	cohl_ai2.seq
		:					3.3			
	GCGCACTA	ATAC	T C T A G C	TACT	CCTCC	CTTTGT	ACAAG	TAAACA	AGCTTAI	Vaj ority
:.		. 2460		2470		2480		2490	2500	
2451	GCGCACTA	ATAC	TCTAGO	TACT	CCTGC	CTTTGT	A C · A A G	TAAACA	AGCTTA	coht. a12 sed
2451	GEGCACTA	ATAC	TCTAG.C	TACT	CCTGC	CTTTGT	ACAAG.	TAAACA	AGCTTA	a909_ai2.seq
. •					•	•			. •	•
	AGTCCCAA	,	. 01016		OUCAG:	• •	AAACT	•	ATUGUTI	lajority
	<u> </u>	2510		2520	<u>. : .</u>	2530		2540	2550	
2501	AGTCCCAA	TCAT	TGTCTG	ATGT	GGCAG	TTTAT	AAACT	TTTCA	ATCGCT	cohi_al2.seq
2501	AGTCCCAA	LUAT	IGTCTC	ATGT	GGCAG	ETTTAT	A A A C. T	TTTTCA	ATCGCT	a909_a12.seq
	GTTGGTTC	AATA	ATTTĊT	CTAT	TACTG	TTTTG	TAGTE	ATAGAT	TT6000	latority .
		2560		2570		2580				agor i cy
2554	· · · · · · · · · · · · · · · · · · ·		1 m m m a -	1	 			2590	2600	
.2551 2551	G T T G G T T C G T T G G T T C	ATAA	ATTTCI	CTAT	TACTG	ATTTTG	TAGTG	ATAGAT	TTGCCCC	ohl_at2.seq
		· · · ·		UIAI			and I G	niaGAT	1 1 6 6 6 6 6 8	isus_aiz.seq

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ar.			114/	487	
Thur	ment Report o sday, July 29, :WO 2006,	/078318 in meth with Weigh	hted residue weight table.	1 *	PCT/US20
•	TGTTGT AnGILLT	G T A A A A F A A A A A A A A A A A A A A		TCTACATTTTT	T A A A G Wajority
2601	TGTTGTAGTT	GTAAAATAACA	Z630 TCCGTTCCCATA	2640 TCTACATTTT	2650 T A A A G cohl al2 seg
2601	IGTTGTAGTT	GTAAAATAAACA	TCCGTTCCCATA	TCTACATTTT	TAAAC a909_a12.seq
	CATCAAATG	A.T A A G G A A A A T T		CACCATGTTAT	TAGTT Majority
2651	CATCAAAAT G	ATAAGGAAAATT	2680	2690	2700
2651	CATCAAAATG	ATAAGGAAAATT	ATGCGCACAAAT	CACCATGTTAT	TAGTT coht_ai2.seq TAGTT a909_ai2.seq
	AAATAAGAAC	CATAATACCTTG	TAGGCGTTTTAG	ACAGTTGTTCA	A A A C T Majority
2701	271 A A A T A A G A A C	2,20	2730	2740	2750
2701	AAATAAGAAC	CATAATAGCTTG	TAGGCGTTTTAG	A C A G T T G T T C A A C A G T T G T T C A	A A A C T coh1_a12.seq A A A C T a909_a12.seq
		GCTACCGGTAAA			
2751	2760	0 2770	2780	2790	2800
2751	ATÄATTAGCA	G C T A C C G G T A A A T G C T A C C G G T A A A T	T G C A G T T T T A A G T T G C A G T T T T A A G T	T T C G G A A T A T C T T C G G A A T A T C	CAGAG cohl_ai2.seq CAGAG a909_ai2.seq
		ATCTGTTTTATC			
2801	2810	2820	2830	2840	2850
2801	TTCCCAAGTA TTCCCAAGTA	A T C T G T T T T A T C (A T C T G T T T T A T C (C A A C T T T T T T A C A	G G T A A T T C T C C	CATTT cohl_al2.seq CATTT a909_al2.seq
•	TCTGAACCCT	TTACTTGATGCGT	AATAGATTATC	•	* *
	2860	2870	2880	2890	2900
2851 2851	TCTGAACCCT	T T A C T T G A T G C G T T T A C T T G A T G C G T	`	AAGCGCCTTG	A C A A T cohi_ai2.seq
	ATGCTGAGAAC	•	GATGCGCCTGAT		
	. 2910	2920	2930	2940	2950
2901 2901	ATGCTGAGAAC ATMCTGAGAAC	G T T A A A T C A G C T T G T T A A A T C A G C T T	GATGCGCCTGAT GATGCGCCTGAT	TAATATTATAC	C A A C cohi_ai2.seq
		C C A G A A C T T A C C			
# 1 00	2960	2970	2980	2990	3000
2951 2951	CCCAATAGATT	C C A G A A C T T A C C C C A G A A C T T A C C	A G A A T A A T T E C G A G A A T G A T T C C A	A G T A T C G C T A A	AAAA cohl_ai2.seq
:		TCTTCTAATCAC			
	3010	3020	3030	3040	3050
3001 3001	TTTGCTGAATA	T C T T C T A A T C A C T C T T C T A A T C A C	GTCTTCTTCTCC GTCTTCTTCTCC	ATTTTAAAGCCT	ATTA cohl_ai2.seq
•		AGTCCTGACATA			
•	3060	3070	3080	3090	3100
3051 3051		A G T C C T G A C A T A A G T C C T G A C A T A	ATTAGTATAGGT	ATTGGCCACCA	TACT cohl_ai2.seq
. : ` `		CGGGAGCTTTCC			
	3110	3120	3130	3140	GAGT Majority
3101 3101	TGTCCAGTAAA	CGGAAGCTTTCC	CTTTGTCTGATG	TGTTACTGTAG	
.•		CGGGAGCTTTCC			
	3160	CTTTTTTAGGTT	TAGCATTTAAAG 3180	G G C T C A T T T T C	T C A A Majority 3200
3151	AATTGTCTCTT	CTTTTTTAGGTT	TACCATTTALAC	000000000000000000000000000000000000000	<u>-</u>
•		o i i i i i i i i i i i i i i i i i i i	I A G C A I I I A A A G	G G C T, C A T T T, T C	T'C A. A. a909_a12.seq
		TCGTACTTCCCA	TCCTTACGTATT:	• ,	4
3201	ATGCTGTAATA	TCGTACTTCCCA	TCCTTAGGTATT	3240 G A T A G T A T A A A	G G G A cohi at2 seg
3201	ATGCTGTAATA	TCGTACTTCCCA	TCCTTAGGTATT	GATAGTATAAA	G G G A a909_a12.seq

			11-11-		
Align	ment Report of $WO~2006/078318$ in met sday, July 29, 2004 6:49 PM	hod with Weighted residue	115/4% weight table.	1	PCT/US200
	GACATIFACTTCAFAIAGE	TT GIA GICIE GIT	TAGTCTCAA	T A A T A G A T A A	A T Wal- 11
	3260	3270	3280	3290	3300
3251 3251	· · · · · · · · · · · · · · · · · · ·	TTGAGCTGTT TTGAGCTGTT	T T A G T C T G A A T T A G T C T G A A	T 4 4 4 T 4 C 4 T 4 4	4.50
	CCCTTGAGGAAGATTGT	TCGCAACAAT	ACCTTCAGCC	G G T A · A A T T A T C	A A Majority
	3310	3320	3330	3340	3350
3301 3301	o o o o o o o o o o o o o o o o o o o	ICGCAACAAI	ACCITCAGCC		A A a909_a12.seq
	ACGTTTGTAAAGGTTGA		CAGCTTTTGT	TAGTAGATTGA	C G Majority
3351	3360	3370	3380	3390	3400
3351		MITTTATGAA	CAGCTTTTGT	TAGTAGATTGA	
	TATTEGETTGETTACT		• •	SATCATCGTCT	T T Majority
3401	TATTTECTTTCCTTACT	3420·	3430	3440	3450
3401	TATTTGGCTTGGTTACT TATTTGGCTTGGTTACT	ATCAA.GGTTT	A C T T G T G T T A E	3 A T C A T C G T C T A A T C A T C G T C T	T T cohi_ai2.seq T T a909 ai2.seq
•	TATTCCAATACCTTGAA				-
	3460	3470	3480	CTTGGTTACC 3490	3500
3451 -3451	TATTCCAATACCTTGAA	ATGGGGTAGT	TAGAGTAAAA	CTTGATTACC	<u></u>
-5451	THE THE COLL OF THE THE	RIGGGGIAGI	LAGAGTAAAAA	CTTGGTTACC	A T a909_a12.seq
	CAACATCTTAGCTTGT	GCTACTTGGT.	AAACAAGTAAA	TTACCGCCAG	C G Majority
3501	CAACATCTTTAGCTTGT	3520	3530	3540	3550
3501	C A A C A T C T T T A G C T T G T C A A C A T C T T T A G C T T G T	GCTACTTGGT. GCTACTTGGT.	A A A C A A G T A A A A A C A A G T A A A	TTACCGCCAG	C G coh1_a12.seq C G a909 a12.seq
	ATACCTTGATTATTATA				
•	3560	3570	3580		.3600
3551 3551	ATACCTTGATTATTATA	CT.TATTT.GT.	ATAGTAATAGA	1.00000	
	ATACCTTGATTATTATA CTGATCATTGGTATCAG	CLIKITITETA	ATAGTAATAGA	ACCCGTTTTC	A T a909_a12.seq
•	. 3610	3620	3630	3640	3650
3601 3601	CTGATCATTGGTATCAG	CAGACACAAG 1 CAGACACAAG 1	T T G A G T A C T T A T T G A G T A C T T A	CACTALATA	
	AGAGAAGAGTTATCTTT	GGATCTTTT	TATAAATCATT	GTTCTCTTCC	FT Majority
	3660	.3670	3680	3690	3700
3651 3651	A G A G A A G A G T T A T C T T T A G A G A G A G A G T T A T A T T T T	GGATCTTTT	ATAAATCATT	GTTCTCTTCC	T T coh1_a12.seq
	TCTCATTGCTTGTTTTAA	3720			•
3701	TCTCATTGCTTGTTTTA		3730 C C T T C A C C T C	3740	3750
370 i	TCTCATTGCTTGTTTA	AATTTTCTTA	CGTTGACGTG	CTCTCCTAGT	A cont_at2.seq
	CTTCTAAAGAGATTAAAA		•		
	3760	3770	3780	3790	3800
3751 3751	CTTCTAAAGAGATTAAAA	GTAAAATCAA	AGTAAGGAAA	ATAGCGATAAA	T cohi_ai2.seq
<i>.</i>	O I TO I A A A A A A A A A A A A A A A A A A	GIRVAVICAV	AGTAAGGAAA	A.T.A.G.C.G.A.T.A.A.A	T a909_a12.seq
-	GGTGCGATATAAATAGGG			TACTACCAAAG	C Majority
3801 .	3810 C C T C C C A T A T A A A T A C C C	3820	3830		3850
3801	G G T G C G A T A T A A A T A G G C G G T G C G A T A T A A A T A G G C	CIALLEGIA	TTGCCTCTGC	TACMACCAAAG	C a909_ai2.seq
	<u>ETTACCATTATCGTTTGG</u>		CCTCTCACTA	G T A A C C G A T G G	<u>G</u> Majority
3851	GTTACCATTATCCTTTCC	3870 TACACCATC	3880		3900
3851	G T T A C C A T T A T C G T T T G G G T T A C C A T T A T C G T T T G G	TACACGAIGT	CCTCTCACTA	G T A A C C G A T G G G T A A C C G A T G G	G cohl_a12.seq G a909_a12.seq

Thurs	day, July 29, 2004 6:49					
	TATTAGE	CATATGGT	GTACACOTCA	CCAAAGTTTGG	TAGTCTTTACC	T Majority
	n. ""	3910	3920	3930		•
2001	T 1 T T 1 1 C C			_		950 1
3901	TATTAACE	CCATATGGT	GTACACGTCA	CCAAAGTTTGG	TAGTCTTTACC	T cohl_ai2.seq
0001	I II I I I I I I I I	ICCKIKIGG1	GIACACGICA	CCAAAGTTTGG	TAGTCTTTACC	T a909_a12.seq
	TTAACAAT	TTGTAAATC	CCTCAAATCA	TCCCCTTTLLC	TGTTCTGATTT	
-					•	Majority
		3960	3970	3980		000
3951	TTAACAAT	TTGTAAATC	CCTCAAATCA	TCCGGTTTAAC	TGTTCTGATTT	C cohi ai2.sea
3951	TTAACAAT	TTGTAAATC	CCTCAAATCA	TCCGGTTTAAC	TGTTCTGATTT	G a909_a12.seq
				and the second s		
	RICCACII		AIGIIICATT	TAAGATACTGA	CTGTCCAGTGG	L Majority
	. <u>- </u>	4010	4020	4030	4040 40	050
4001	ATCCACTT	GATAAGTAT	ATGTTTCATT	TAAGATACTCA	CTGTCCAGTGG	L
4001	ATCCACTT	GATAAGTAT.	ATGTTTCATT	TAAGATACTGA	CTGTCCAGTGG	T a000 at2 seq
			•			-
	CTCCAGCT	TTTAACTTA.	FCCAAATCAG	AAAAAGCCTT	GAAGAGGGTAAA	A Majority
:		4060	4070	4080		00
4051	CTCCAMCT	TTTAACTTA	TCCAAATCAC	_		
· 4051	CTCCAGCT	TTTAACTTA	T C C A A A T C A C	AAAAAAGCCTT	GAAGAGGGTAA.	A cohi_ai2.seq
			. CONNECTOR	A A A A A G C C I I	G A'A G'A G G G I A A I	A a909_a12.seq
	CCTCTATG	TCCTGATAAA	AATAGAATGA	GTTGAGTCTCC	TCCAATTGGAA	. Walocity
		4110	4120	4130	•	, -
4101	0.0 0.0 0.0 0.0			•		50 L
4101		TCCTCATAL	A A T A G A A T G A	GTTGAGTCTCC	TCCAATTGGAAG	G cohl_ai2.seq
1201	, our or a re-	COLGALRA	MAIAGAAIGA	GITGAGTCTCC	T-C C A A T T-G G A A	G a909_a12.seq
. •	ACTACTTC	CTTCTAAATC	ACCAATAGA	AGTTTGAACCA	CTTTTTCACTTC	Valantai.
	•	4160	4170	•	•	
40-6	100100	4	-	4180		00
4151 4151	ACTACTTC	CTTCTAAAT	GACCAATAGA	AGTTTGAAGCA	CTTTTTCACTT	cohl_ai2.seq
	"OINOIIC	CITCIANAI	ACCARIAGA	A G I I I G A A G C A	CTTTTCACTT	3 a909_a12.seq
	TACCATGA	TAAAGTGGTA	ATTTTATGT	TTATCTTTGGA	ATTGAAATATAA	Majority
		4210	. 4220	.4230		
4201	TACCATCA	TAAACTCCT	•			
	TACCATGA	TAAAGTGGT		TIAICITTGGA. TTATCTTTCCA	ATTGAAATATAA ATTGAAATATAA	cohi_ai2.seq
		*		•		• •
	CCCATATT	A C C C G T T T T A	TCGATAGCC	AGTTGTGAATT	ATAATCCAAACG	Majority
		4260	4270	4280	4290 439	
4251	CCCATATT	ACCCGTTTTA	TCGATACCC		ATAATCCAAACG	
4251	·CCCATATT	ACCCGTTTTA	TCGATAGCC	A G T T G T G A A T T	A T A A T C C A A A C G	cohl_ai2.seq
			•			-
	CTCTTGGT	TAGTCATGTG	CCACTTCATT	FCCTGAAGTTT	TAAATTGCTTAT	Majority
	•	4310	4320	4330	4340 43	
4301	CTCTTCC	TAGTCATCTC	CCACTTCAT	FCCTCAACTT	TAAATTGCTTAT	
4301	CTCTTGGT	CAGTCATGTG	CCACTTCAT	T C C T C A A C T T T	TAAATTGCTTAT	cohl_ai2.seq
•						
	TATATTCT	TTGGCTCGGT	TAATAATTT	TTTTATAGTCG	TTTTCATCCATA	Majority
			4370	4380	4390 440	
4351	TATATTET	TTGGCTCGGT	TA AT A A TIT T	T T T T A T A T A T T C C	TTTTCATCCATA	
4351	TATATTCT	TTGGCTCGGT	TAATAATTT	r i i i i i i i i i i i i i i i i i i i	TTTTCATCCATA	cohl_ai2_seq
• •						
٠.	TGCGTTAC	GCGGTCTTGG	TAATCGATAA	TCGCTCGAGA	TTGGTGAAATGA	Majority
		4410	4420	4430	4440 445	• •
4101	TCCCTTA					
4401	TECETTAC	6	TAATUUATAA	TCGCTCGAGA	TTGGTGAAATGA	cohi_ai2.seq
•		0000101144	TARICCALM!	CICGCICGAGA	TTGGTGAAATGA	a909_a12.seq
_	ATTCCAAT	AATTAGCAAG	TGAAGGATAA	G C C A T T A A G C (CTACCCCCACTG	Valority
	•	4460	4470			
	A m m o o o o o				4490 450	•
4451	ATTCCAAT	AATTAGCAAG	TGAAGGATA	GCCATTAAGC	CTACCCCCCACTG	cohi_ai2.seq
4451	ALICUARI:	natino CAAG	IUAAUGATA	A G C C A T T A A G C (CTACCCCCCACTG	a909_a12.seq
	CAATTATAC	G T G A C A A C C A	AAATGGATAC	TAAATCTTCT	CTTATTTTTTC	/ Valàntes
-						- wajority
-		-	•			
	·	4510	4520	4530	4540 455	
4501 4501	CAATTATA	4510 G T G A C A A G C A	4520 A A A T G G A T A C	4530 C T A A A T G T T G T 6		cohi al2 coa

Align Thus	ment Report of W) 2006/078318	in method with Weighted r	$117/4^3$ residue weight table.	87	PCT/US20
	ATATATA			TEETACCCCAT	CTTATTAAGAA	CGTA Majority
4		4560	4570	4580	4590	4600
4551 4551	ATATAT	TTTAAATC	TGTACCACTT	TGCTAGCCCAT	CTTATTAAGAA	C G T A cohl_al2.sec C G T A a909_ai2.sec
	AACGACO	ACGAGCA.		TACCTGCTCCTA	TTACTAAAAT	TGCA Majority
4601	AACGAC	4610 GACGAGCA	A C A A G C A C G A	4630 TACCTCCTCCT	4640	4650
4601	AACGAC	GACGAGCA	A C A A G C Á C G A	TACCTGCTCCTA		TGCA coh1_a12.seq TGCA a909_a12.seq
	CCTATAA	TGTAGAA	AATTGTTGTA	CCAATACCACCT	GTTGAAGGCA.	ACTC Majority
AGE 1	CCTATA	4660	4670	4680	4690	4700
4651	-			C C A A T A C C A C C T C C A A T A C C A C C T	GTTGAAGGCA GTTGAAGGCA	A C T C cohi_al2.seq A C T C a909_al2.seq
	AGTACCT	TTGTTATT	TTTCAACAGT 1	T G G G T T A A C T A A	AAGGTTATCT	GAAT Majority
1701	AGTACCT	4710 TTGTTAT1	4720	4730	4740	4750
4701	AGTACCT	TTGTTAT	·······································	T G G G T T A A C T A A T G G G T T A A C T A A	AAGGTTATCT	GAAT a909_ai2.seq
	TAGTCGT	A T C A G T G G		C T A A A A T A A C C T	TCTGAGAGTT	TCT Majority
4751	TAGTCGT		4770.	4780	4790	4800
4751	TAGTCGT	ATCAGTGG	CTCCATCTCC	TAAAATAACCT	•	T C T a909_a12.seq
	AACAAAT	TGTAACCT		TTTTCTCAACT	AGATAGTATGT	A.C.C Majority
1801	AACAAAT	4810 T.C.T.A.A.C.C.T	A A G G G A G C C T	4830	4840	4850
801	AACAAAT	TGTAACCT	AAGGGAGCCT	TTTTCTCAACT	AGATAGTATGT	ACC cohl_ai2.seq ACC a909_ai2.seq
	TTCTTTC		•••	ATACCATCTCC	TCCTGTTGTAT	ATT Majority
8 51	TTCTTTC	4860 A A C C C T C T	4870	4880	4890	4900
851			WW. TOO TAATI	ATACCATCTGC ATACCATCTGC	T C C T G T T G T A T T C C T G T T G T A T	ATT cohl_ai2.seq ATT a909_ai2.seq
	CTGTTGC	<u>A T T A G C T T</u> 4910	• •		TTGTATCGTTA	A A G Majority
901	CTGTTGC		. 4920	4930	4940 .	4950
901			o i d i d c c c x	T T C A A C G T T A T T T C A A C G T T A T	TIGTATEGTTA	A A G a909_ai2.seq
	TITAGAA	4960	GTAGCATTCT 4970	TTAAAACAAAT	•	T A A Majority
951	TTTAGAA	ATTGACCC	GTACCATTCT	4980 T _. T A A A:A C A A A T	4990 A T A C C A C C T T C	5000
951			GTAGCATTCT	TTAAAACAAAT	ATAGCACCTTG	T A A cohl_a12.seq T A A a909_ai2.seq
• • •	IGAAGUI	. 5010		TTTTTATAGT	AATTTGACCAT	C C C Majority
101	TGAAGCT		5020	5030	5040	5050
			ACCALCAAII.	TTTTTTATAGT:	A'A T T T'G A C C,A'T	C C C a909_ai2.seq
	ICACIGI	FOCO		ATCATTECTAGT	FATTGGGGTTG:	ATC Majority
)51	TCACTGT	5060 CACTTTT	5070	5080	5090	5100
:			UKCCIGGGIC.	ATCATTGCTAG ATCATTGCTAG	LVLLCCCCLLC	A T G a909_a12.seq
. :	GTCG'CAA1	GTTTGTA	T.TTCTGGTA	AATCAGCTGAAC	CTGGTTTAGC	TCC Majority
01	GTĆCCAA	5110	5120	5130	5140	5150
		·····	I I I I C I G G I A	A A T C A G C T G A A C A A T C A G C T G A A C	CTGGTTTAGC	T C C a909_a12.seq
	ACTCTTTA	ATACTCCT		A C T G T G A T T G T A	TTTATTCCCT	TAT Majority
_	<u> </u>	5160	5170 . 1	5180 ·	5190	5200
151 151	ACTCTTTA	ATACTCC	I G T A T A A G T G A I G T A T A A G T G A	A C T G T G A T T G T A A C T G T G A T T G T A	TTTATTCCCT	TAT cohl_a12.seq TAT a909_a12.seq

	•					
Aligr Thur	ument Report o WO 200 Sday, July 29	6/078318 ^{in mett}	noo with Weighted residue	118/487 weight table.	1	PCT/US200
-	A A A A A A A G	CATCATIA			GGTTGGAGTAT	T G Majority
520	· •	CATCATTA	5220	5230 ·	5240	5250
520	I AAAAAAGT	CATCATTA		G A G T A T T T C C G A G T A T T T C C		T G cohl_al2.seq T G a909_al2.seq
		•	AGTAATCGTG	A A A T T A T T A A A	TTTCCTCTAAC	A G Majority
5251	GTAGCTGCC	CACGGAAT	AGTAATCGTG	5280 A A A T T A T T A T	5290 T.T.T.C.C.T.C.T.A.A.G	5300
5251	GTAGCTGCC	CACGGAAT	AGTAATCGTG	AÁATTATTAT	TTTCCTCTAAC	A G cohl_a12.seq C A G a909_a12.seq
	GTTATACTT	CCCAGTTG	CTTTTTCCGA 5320		AGAGTTGTAAT	A T Wajority
5301	GTTATACTT	CCCAGTTG	CTTTTTCCGA	5330 ACCTTGAGTT	5340 AGAGTTGTAA1	5350
5301			CITITICCGA	ACCTTGAGTT	AGAGTTGTAAT	A.T a909_ai2.seq
		CATCAGTA 360	ATAGTTACTT 5370	CATAAGATCC 5380		T
5351	TCCCTGATC	CATCAGTA	ATAGTTACTT	CATAACATCC	TTCGTTCAAAT	5400 C.A. cohi ai2 sag
5351		ORICANGIA,	RINGIIACII	CATAAGATCC	TTCGTTCAAAT	C A a909_a12.seq
		GCAGATGG (5420	TTATAACAT 5430	ATTGATACACT	
5401	ACTACAGAA	GCAGATGG	CATAGTATCC	TTTATACAT	5440 ATTGATACACT	5450 T T coh1_ai2.seq
5401	ROINGROAM	G C.A G A I G G (ATAGTATEC	TTTATAACAT	ATTGATACACT	T T a909_a12.seq
•	54	60.	GACTGCATT	STTATAAGTA	<u> </u>	•
5451 5451	TTCTGTACC	A T G A T A A T 7	GACTGCATT	CTTATATATA	T 4 C:T 4 T 4 T 7	5500 G A coh1_a12.seq
0.01				CTTATAAGTA		G A a909_a12.seq
	55	10	5520	5530	TTTCCACCAC.	<u>C A</u> Majority 5550
5501 5501	CTGTATCAC	AACCGAGT	ACGTTTTTT	ATCTACAGT	TTTCCACCAC	
-					AGCATTTGGA	
· · .	55	60	5570	5580	5590	5600
5551 5551	TCTCCCCATC	TCGCATCA TCGCATCA	GTATTCTTTT GTATTCTTTT	CATGAATAG	A G C A T T T G G A	G T cohl_al2.seq
	•			-	TGCTAGAAAC	-
	56	10.	5620	5630	5640	5650
5601 5601	TACAGATGTA TACAGATGTA	A C C A T A A T A C C A T A A T	CACAGCTCCA TACAGCTCCA	TTATTAACAG TTATTAACAG	T G C T A G A A A C T G C T A G A A A C	A T cohl_ai2.seq
				AACCTCAGTA		<u>r T.</u> Majority
ECE 1	560	io	5670	5680	5690	5700
5651 5651	AATAATATCC	ATATTGGG ATATTGGG	A A A C A T T A A T A A A C A T T A A T	AACCTCAGTA AACCTCAGTA	C C A T C A T T A T	T T cohl_a12.seq
: :					TATAGATTTA	
ĖTOT	571	0	5720	5730	5740	5750
5701	GACTCAGTAA	CAGTGGAA	ACTGGTGTAG ACTGGTGTAG	TATTAGCTGA TATTAGCTGA	TATAGATTTA	C cohl_a12.seq
					TAGTTACATA1	
5751	576	0	5770	5780	5790	5800
5751 5751	CCATGTCGCA	ATCTCATT	I G C T G A C G C A T G C T G A C G C A	GTATCTTTT GTATCTTTT	TAGTTACATAT	f G cohl_ai2.seq . f G a909_ai2.seq .
					A A A T C A G T T G A	
5801	581	0	5820	5830	5840	5850
5801	TTCTCCCTCC	ATTAGTAG	I PGTCGTAAA TTGTCGTAAA	A A G A G A A T T A A A G A G A A T T A	A A A T C A G T T G A A A A T C A G T T G A	A cohl_ai2.seq A a909_ai2.seq
	•		•			-

	_			1101.		
Alignr	nent Report CWO	2006/078318 in m	ethod with Weighted res	idue weight table.	7	PCT/US200
•inuis	ady, odly 20, 2004 0.	A'O'T CA GIC'N'I			TAAGAAGCTCCA	T.C. Valority
	16 3111	5860	5870	5880	5890	5900
5851 5851	GCTTTAT	A C T C A G C T T A C T C A G C T T	C T T T A C C T T C T T T A C C T T	G A G G A A T T A A A G A G G A A T T A A A	T A A G A A G C T C C A T A A G A A G C T C C A	T C cohl_ai2.seq T C a909_ai2.seq
	TTTATTC		ACATTTGCA	TTATCTATTTC	TGCATCAAAAC	TT Wajority
5901	TTT	5910 C A A T C A C A T	5920	5930	5940	5950
5901	LILKITO	OKKICKGKI.	ACATIIGCA	TTATCTATTTC	T G C A T C A A A A A C T G C A T C A A A A A C	T T a909_a12.seq
	TGTATGC			•	G A A C T G T A A T T G	T C Wajority
5951	TATATEC	5960 TTTATACCT:	5970	5980	5990	6000
5951	ISTRIGO	III, AIAGGI	IGCGCCTTT	TTGAGTATCTT	G A A C T G T A A T T G G A A C T G T A A T T G	T C a909_a12.seq
	CCTCTCTC	6010		•	GATACAGCCATA	C C Najority
6001	CCTGTCT		6020 A A C C T A T C C	6030	GATACAGCCATA	6050
6001	CCTGTCT	CAGCGGCAA	AGCTATCG	GCGTAACTGGT	G A T A C A G C C A T A	C C cohl_a12.seq C C a909_a12.seq
-	AAATGCTA	AACTCGCC!	CTAACAGC	GATTGAATCAT1	TTTCTTTTTCAT	T G Kajority
		6060	6070	6080	6090	6100
6051 6051	AAATGCT	A A C T C G C C A A A C T C G C C A	A C T A A C A G C	G A T T G A A T C A T T G A T T G A A T C A T T	TTTCTTTTTCAT	T G cohi_ai2.seq T G a909_ai2.seq
	AAATCTTI	CTCCTAAAA	TCATATTG	ATGAATGATTA/	ATTCATATTTTT	T T Majority
		6110	6120	6130	. 6140	6150
6101 6101	AAATCTTI	CTCCTAAAA CCTCCTAAAA	T C A T A T T G	A T G A A T G A T T A A A T G A A T G A T T A A	A T T C A T A T T T T T A T T C A T A T T T T T	T T coh1_a12.seq T T a909_a12.seq
	TCGATAGI		ATCCTGATO	G T A G À G C'T A A A	GCTAAACCAAC	T.A Majority
C1E1	T.C.C.A.T.A.G.T	6160	6170	6180	6190	6200
6151	TCGATAGI	ATTATATAT	ATCCTGAT	G G T A G A G C T A A A G G T A G A G C T A A A	A G C T A A A C C A A C . A G C T A A A C C A A C .	T A cohl_ai2.seq T A a909_ai2.seq
	GGATATAA	ATGTGTGTT	CCAATACCI	CCAGTACTAGG	CAATTCTGTTC	C T Majority
6201		6210	6220	6230	6240	6250
6201 6201	GGATATAA	ATGTGTGTT	CCAATACCT	C C A G T A C T A G G C C A G T A C T A G G	C A A T T C T G T T C C	C T cohl_ai2.seq C T a909_ai2.seq
	TTACTGTT			TACTGTACTTC	CATCTACTAAA	CT Majority
6251	TTACTGTT	6260 AGTAATTT	6270	6280		6300
6251	TTACTGTT	AGTAATTT	A A A A G T.A T A	TACTGTACTTC	CATCCACTAAA1 CATCTACTAAA1	TT a909_a12.seq
					AAGGTAACTCCC	C Majority
6301		TTGGTGTCG	6320 CATTATTAC	6330	AAGGTAACTCC	6350
6301	CTCTTTA	TTGGTGTCG	CATTATTAC	CATTTTGTTCA	AAGGTAACTCCC	CG cohl_ai2.seq CG a909_ai2.seq
					TAGGTACCCTGG	· .
		6360	6370	6380		6400
6351 6351	TAGAAATC	ACTAATACT ACTAATACT	G A T A T A T C A G A T A T C A	TTTTTAGGTAG TTTTTAGGTAG	TAGGTACCCTGG	A cohl_ai2.seq
•	GGGGCCTT	т. с т с т с т с т	TAGGTAGTA	TTTTCCTACTG	GCAAACTGAGGT	A Vajority
	•	6410	6420	6430	6440	
6401 6401	GGGGGCCTT	TGTCTCTGT TGTCTCTGT	T	TTTTCCTACTG TTTTCCTACTG	F D D A D T D A A A D D T D A A A A D D T D A A A A	f A cohi_ai2.seq f A a909_ai2.seq
			•		GTCACCAGCCCT	
•	<u> </u>	6460	6470	6480	6490	6500
6451 6451	G T T A T T A G G T T A T T A G	CATCCACTA CATCCACTA	A T A A C A A G C A T A A C A A G C	CTTTATCGTTT CTTTATCGTTT	G T C A C C A G C C C T G T C A C C A G C C C T	G cohl_ai2.seq G a909_ai2.seq

	130ay, July 29, 2004 6:49 P			41711)		
	AATACATA	GATOT C	ASC DIT TAIT	COCATTAGCA	TCTGATTCAT	A A A T A Majority
		6510	6520	6530	6540	•
650	1 AATACATAC	GATGTG	ACCTTTATI		0340	6550
650	1 AATÁCATA (GATGTGA	AGCTTTATT		TCTGATTCAT	A A A T A cohi_ai2.seq A A A T A a909_ai2.seq
	TCAAAAACT	GCACCTO	CTAAAAAAAT	TATTATCATT	TTCGACATTA	A C T T T Votonites
	*	6560	6570	- 6580	-	•
655	T C A A A A A C T	CCACCTO			6590	6600
6551	TCAAAAACT	GCACCTG	CIARAAAAI	TATTATCATT	TTCGACATTA	ACTTT cohl_ai2.seq ACTTT a909_ai2.seq
				TATIAICALT	TTCGACATTA	ACTTT a909_a12.seq
	CTGTAGTCG	TACTTTT	TGCTTGATA	CGTGTATTGG	TAAACCTAAT	ATCTA Mata-ta-
	•	5610 .	6620	6630	•	
6601	CTGTAGTCG	TACTTT			6640	6650
6601	CTGTAGTCG	TACTTTT	IGCTTGATA	CGTGTATTGG	TAAAGCTAAT	ATCTA cohi_ai2.seq
	•		TOOLIGAIA	COLGIALLEGG	TAAAGCTAAT	ATCTA a909_a12.seq
	CCTCTCCTG	AAACTGT	CAGGGATTG	TAAGCCGGTA	CCATCATAAC:	PTT T A Maranta
	•	6660	6670	6680	-	•
6651	CGTCTCCTC	1 4 4 6 7 6 7	•		. 6690	6700
6651	CGTCTCCTG	AAACTGI AAACTGT	DAGGGATTG	TAAGCCGGTA	GCATCATAAG	TTTTA coh1_ai2.seq
						TTTTA coh1_ai2.seq TTTTA a909_ai2.seq
-	TCAGCTTCA	CCAGTTG	CTAGATTTT	TTTCTGTAAT	T G A C T C A C A T A	LCTTT W
		710	6720			CIII Majority
6701				6730	6740	6750
6701	TCAGCTTCA	CCAGTTG	CTAGATTTT	TTTCTGTAAT	TGACTCAGATA	CTTT cohl_al2.seq
		CCAGIIG	CIAGAILTT	TTTCTGTAAT	TGACTCAGATA	CTTT cohl_al2.seq CTTT a909_al2.seq
	AAATTCATC	GTAGGCT	TGTTCATCT	ATTGATATAG	A A C T T C C A T A A	0.0 7 4 4 4
	6	760	6770		•	GGTA Majority
6751		•		6780	6790	6800
6751	AAATTCATC	GIAGGGT	TGTTCATCT	ATTGATAG	AAGTTCCATAA	G G T A cohi_ai2.seq
••				ALIGNIALAG	RAGIICÇATAA	GGTA a909_a12.seq
	CTTTKAATT	CCTTAGT	CTGACCATC	TCTCAGCGGA		TTCCIV
	6	810	6820		• •	11 GC Majority
6801				. 6830	6840 :	6850
6801	CTTTAAATT	CCTTAGT	C T G A C C A T C	TCTCKGCGGA	LAATTCTCTTTG	TTGC cohl_ai2.seq
			· ·	ICICAGOGGA	AAATT CTCTTG	TTGC cohl_ai2.seq TTGC a909_ai2.seq
	AACGTTTCA	CTTGGAT	TAAACAAGA	AGTCTTTCGTC	. TTATCTTCAT	CTACKE
	68	360.	6870	6880	•	CTAG Majority
6851	AACGTTTCA	CTTCCAT			6890	6900
6851	AACGTTTCA	CTTGGAT	TAAACAAGA,	A G T C T T T C G T (TTATCTTCAT	CTAG cohl_ai2.seq CTAG a909_ai2.seq
	TCCAACGAC	GTTTTA	CTTACTCTGA	ACGGTGTATTC	TTTAGGTTGC	C A A A Votonitu
	. 69	10	6920	6930	•	•
6901	T.CCAACGAC	AGTTTTA	CTTACTCTC		6940	6950
6901	TCCAACGAC	AGTTTTA	CTTACTCTC	A C C C T C T A T T C	TTTAGGTTGC	C A A A coh1_a12.seq C A A A a909_a12.seq
•						
	CAGCATATA	GGTATTT	T G T T G C A T C A	GGGTTGTTAT	CAATACCTAT	T G A T Majority
	. 69	60	6970	6980	6990	•
6951	CAGCATATA	GGTATTI	CATTCCLTC	1000000000		7000
6951	CAGCATATA	GGTATT	CTTGCATCA	V G G G T T G T T A T	CAATACCTAT	T G A T cohl_ai2.seq T G A T a909_ai2.seq
				. d.a.a.r. a.r.a. V. I	CAALACCTAT	T G A T a909_a12.seq
•	TGACCTGCTC	TAAATTC	CACACGTCC	TGTATCAGCT		
					AAATCCTTAT	C. A. T. C. Valoritie
7001	70	10			AAATCCTTAT	
700 L	70	10	7020	7030	7040	7050
	TGACCTCCT	10 TAAATT <i>(</i>	7020	7030	7040	7050
	TGACCTGCTG TGACCTGCTG	TAAATTC	7020 C A C A C G T C C C A C A C G T C C	TGTATCAGCT	7040 AAATCCTTAT	7050 C A T G cohl_ai2.seq C A T G a909_ai2.seq
	TGACCTGCTG TGACCTGCTG	TAAATTC	7020 C A C A C G T C C C A C A C G T C C	TGTATCAGCT	7040 AAATCCTTAT	7050 C A T G cohl_ai2.seq C A T G a909_ai2.seq
	TGACCTGCTG TGACCTGCTG	10 T A A A T T C T A A A T T C A T A A G G T	7020 C A C A C G T C G C A C A C G T C G	7030 T G T A T C A G C T T G T A T C A G C T T C C T T G T A A A	7040 A A A T C C T T A T A A A T C C T T A T G T A T T G G T T T	7050 CATC cohl_ai2.seq CATC a909_ai2.seq TCAC Majority
	TGACCTGCTGTGACCAACCA	10 TAAATTC TAAATTC ATAAGGT	7020 C A C A C G T C C C A C A C G T C C T G T A A C C T G 7070	7030 C T G T A T C A G C T C T G T A T C A G C T T C C T T G T A A A 7080	7040 A A A T C C T T A T A A A T C C T T A T G T A T T C G T T T 7090	7050 CATG cohl_ai2.seq CATG a909_ai2.seq TCAG Majority
7051	70 T G A C C T G C T G T G A C C T G C T G A T G C C A A C C A 70 A T G C C A A C C A	10 T A A A T T C T A A A T T C A T A A G G T	7020 C C A C A C G T C G C A C A C G T C G T G T A A C C T G T070	7030 CTGTATCAGCT TGTATCAGCT TCCTTGTAAA 7080	7040 A A A T C C T T A T A A A T C C T T A T G T A T T G G T T T T 7090	7050 CATG cohl_ai2.seq CATG a909_ai2.seq TCAG Majority 7100
7051 7051	TGACCTGCTC TGACCTGCTC ATGCCAACCA TOO ATGCCAACCA ATGCCAACCA	10 T A A A T T C T A A A T T C A T A A G G T 60 A T A A G G T A T A A G G T	7020 C A C A C G T C C C A C A C G T C C T G T A A C C T G T G T A A C C T G T G T A A C C T G	7030 C T G T A T C A G C T T G T A T C A G C T T C C T T G T A A A 7080 T C C T T G T A A A T C C T T G T A A A	7040 A A A T C C T T A T A A A T C C T T A T G T A T T G G T T T 7090 G T A T T G G T T T G T A T T G G T T T	7050 CATG cohl_ai2.seq CATG a909_ai2.seq TCAG Majority 7100 TCAG cohl_ai2.seq TCAG a909_ai2.seq
7051 7051	TGACCTGCTC TGACCTGCTC ATGCCAACCA TOO ATGCCAACCA ATGCCAACCA	10 T A A A T T C T A A A T T C A T A A G G T 60 A T A A G G T A T A A G G T	7020 C A C A C G T C C C A C A C G T C C T G T A A C C T G T G T A A C C T G T G T A A C C T G	7030 C T G T A T C A G C T T G T A T C A G C T T C C T T G T A A A 7080 T C C T T G T A A A T C C T T G T A A A	7040 A A A T C C T T A T A A A T C C T T A T G T A T T G G T T T 7090 G T A T T G G T T T G T A T T G G T T T	7050 CATG cohl_ai2.seq CATG a909_ai2.seq TCAG Majority 7100 TCAG cohl_ai2.seq TCAG a909_ai2.seq
7051 7051	70 T G A C C T G C T C T G A C C T G C T C A T G C C A A C C A 700 A T G C C A A C C A A T G C C A A C C A G A A T T G T A G T	10 T A A A T T C T A A A T T C A T A A G G T 60 A T A A G G T A T A A G G T	7020 C C A C A C G T C C C A C A C G T C C T G T A A C C T G T070 T G T A A C C T G T G T A A C C T G T G T A A C C T G	7030 C T G T A T C A G C T C T G T A T C A G C T T C C T T G T A A A 7080 T C C T T G T A A A T C C T T G T A A A A T A C G C G G T G	7040 A A A T C C T T A T A A A T C C T T A T G T A T T G G T T T 7090 G T A T T G G T T T G T A T T G G T T T T C T C T A C T T G.	7050 C A T G cohl_ai2.seq C A T G a909_ai2.seq T C A G Majority 7100 T C A G cohl_ai2.seq T C A G a909_ai2.seq T C A G a909_ai2.seq
7051 7051	70 T G A C C T G C T C T G A C C T G C T C A T G C C A A C C A 70 A T G C C A A C C A A T G C C A A C C A G A A T T G T A G T	10 T A A A T T C T A A A T T C A T A A G G T A T A A G G T A T A A G G T T G T G C T A	7020 C A C A C G T C C C A C A C G T C C T G T A A C C T G T G T A A C C T G T G T A A C C T G T G T A A C C T G	7030 C T G T A T C A G C T C T G T A T C A G C T T C C T T G T A A A 7080 T C C T T G T A A A T C C T T G T A A A A T A C G C G G T G 7130	7040 A A A T C C T T A T A A A T C C T T A T G T A T T G G T T T 7090 G T A T T G G T T T G T A T T G G T T T T C T C T A C T T G 7140	7050 CATG cohl_ai2.seq CATG a909_ai2.seq TCAG Majority 7100 TCAG cohl_ai2.seq TCAG a909_ai2.seq TCAG a909_ai2.seq
7051 7051	TGACCTGCTC TGACCTGCTC ATGCCAACCA TO ATGCCAACCA ATGCCAACCA ATGCCAACCA GAATTGTAGT GAATTGTAGT	10 T A A A T T C T A A A T T C T A A A G G T 60 A T A A G G T A T A A G G T T G T G C T A	7020 C A C A C G T C C C A C A C G T C C T G T A A C C T G T G T A A C C T G T G T A A C C T G T G T A A C C T G T T C A A C T C C T120 T T C A A C T C C	7030 C T G T A T C A G C T C T G T A T C A G C T T C C T T G T A A A 7080 T C C T T G T A A A T C C T T G T A A A A T A C G C G G T G 7130	7040 A A A T C C T T A T A A A T C C T T A T G T A T T G G T T T 7090 G T A T T G G T T T G T A T T G G T T T T C T C T A C T T C 7140	7050 CATG cohl_ai2.seq CATG a909_ai2.seq TCAG Majority 7100 TCAG cohl_ai2.seq TCAG a909_ai2.seq TCAG a909_ai2.seq